

Delaval, Jan

73287

From: Gambel, Phillip
Sent: Wednesday, August 14, 2002 9:59 AM
To: Delaval, Jan
Subject: 09 / 811384

jan

please perform a sequence and a sequence interference search for
09 / 811384

SEQ ID NO: 10

SEQ ID NO: 11

thanx

phillip gambel
art unit 1644
308-3997

Room 8B03

1644:maiblox 9e12

Jan Delaval
Reference Librarian
Biotechnology & Chemical Library
CM1 1E07 - 703-308-4498
jan.delaval@uspto.gov

SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: _____ Examiner #: _____ Date: _____
Art Unit: _____ Phone Number 30 _____ Serial Number: _____
Mail Box and Bldg/Room Location: _____ Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: _____

Inventors (please provide full names): _____

Earliest Priority Filing Date: _____

**For Sequence Searches Only* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

Jan Delaval
Reference Librarian
Biotechnology & Chemical Library
CM1 1E07 - 703-308-4488
jan.delaval@uspto.gov

STAFF USE ONLY

	Type of Search	Vendors and cost where applicable
Searcher: <u>Jan</u>	NA Sequence (#) _____	STN _____
Searcher Phone #: <u>4458</u>	AA Sequence (#) <input checked="" type="checkbox"/> _____	Dialog _____
Searcher Location: _____	Structure (#) _____	Questel/Orbit _____
Date Searcher Picked Up: <u>8/11/02</u>	Bibliographic _____	Dr.Link _____
Date Completed: <u>8/14/02</u>	Litigation _____	Lexis/Nexis _____
Searcher Prep & Review Time: _____	Fulltext _____	Sequence Systems <input checked="" type="checkbox"/> _____
Clerical Prep Time: <u>()</u>	Patent Family _____	WWW/Internet _____
Online Time: <u>()</u>	Other _____	Other (specify) _____

A:Accession: A49444
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-220 <SAU>
A:Note: this sequence modified after extraction from NCBI backbone
A:Note: this sequence report includes corrections based on crystal structure refinement
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
F:137-202/Domain: immunoglobulin homology <IMM>

Query Match 63.5%; Score 782.5; DB 2; Length 220;
Best Local Similarity 69.6%; Pred. No. 1.6e-47;
Matches 158; Conservative 20; Mismatches 42; Indels 7; Gaps 2;

QY 1 EVQLVESGGGLVQPQGGSLRLSCATSGYTFEYTHMMRQAPGKLEWVAGINPKNGTSH 60
DB 1 QVQLQSGFGLVPPSQTLSTCTVSGTSFDDYHWVRQPPGKLEWI-GYVEYTGTTLL 59
QY 61 NORFMDRFTISVDKSTSTAYMQMNSLRADTAIVYCARWGLNYGDFVYFVWVGQGLTV 120
DB 60 DPSLRGRVTLNVTNKGQFSLRLSSVTAADTAIVYCAR-----NLIAGGIDVWVGQGLV 113
QY 121 TVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV 180
DB 114 TVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV 173
QY 181 LQSSGLYSLSSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKVEPKSC 227
DB 174 LQSSGLYSLSSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKVEPKSC 220

RESULT 3
PC4436
monoclonal antibody 13-1 heavy chain - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 04-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 21-Jan-2000
C:Accession: PC4436
R:Kashi, S.; Kato, K.; Torizawa, T.; Dohmae, N.; Yamaguchi, H.; Kamachi, M.; Harada, A.
Biochem. Biophys. Res. Commun. 240, 566-572, 1997
A:Title: Structural characterization of mouse monoclonal antibody 13-1 against a porphyrin
A:Reference number: JC5810; MUID:98063277
A:Accession: PC4436
A:Molecule type: protein
A:Residues: 1-444 <AKA>
C:Comment: This catalytic antibody has peroxidase activity. It is directed against
C:Superfamily: immunoglobulin C region; immunoglobulin homology
F:251-320/Domain: immunoglobulin homology <IMM>
F:22/Disulfide bonds: interchain (to 98) #status predicted
F:99/Disulfide bonds: interchain (to 109) #status predicted

Query Match 56.2%; Score 693.5; DB 2; Length 444;
Best Local Similarity 60.2%; Pred. No. 5e-41;
Matches 139; Conservative 24; Mismatches 55; Indels 13; Gaps 4;

QY 1 EVQLVESGGGLVQPQGGSLRLSCATSGYTFEYTHMMRQAPGKLEWVAGINPK--NGGT 58
DB 1 EVQVETGGGLVPPQNSLKLCLTSGFTSFNRMHLRQPPGKRLNIAVITVKSNDYGA 60
QY 59 SHNRFRDFTISVDKSTSTAYMQMNSLRADTAIVYCAR--WRGLNYGDFVYFVWVGQ 116
DB 61 KYAESVGRFTISRDKSSVYLNQNRRLREEDTATVYCCRTPW-----VYAMDCWQ 112
QY 117 GTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHT 176
DB 113 GTSIVSSAKTTPPSVYPLAPGSAAGTNSMVTLGCLVKGYFPEPVTVSWNSGSLSSGVHT 172
QY 177 FPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKVEPKSC 227
DB 173 FPAVLQSD-LYTLSSSVTVTPSSVWTPSTCNVAHPASSTKVDKKIVPRDC 222

RESULT 4
S38950
Ig gamma chain - mouse
C:Species: Mus musculus (house mouse)
C:Date: 19-May-1994 #sequence_revision 10-Nov-1995 #text_change 16-Jul-1999
C:Accession: S38950
R:Kiebert, S.; Kratzin, H.D.; Zimmermann, B.; Vaesen, M.; Frosch, M.; Weisgerber, C.;
Biol. Chem. Hoppe-Seyler 374, 993-1000, 1993
A:Title: Primary structure of the murine monoclonal IgG2a antibody mAb735 against alp
A:Reference number: S38950; MUID:94128242
A:Accession: S38950
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-246 <KLE>
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
F:137-201/Domain: immunoglobulin homology <IMM>

Query Match 55.8%; Score 688; DB 2; Length 246;
Best Local Similarity 57.8%; Pred. No. 6.6e-41;
Matches 130; Conservative 41; Mismatches 46; Indels 8; Gaps 3;

QY 1 EVQLVESGGGLVQPQGGSLRLSCATSGYTFEYTHMMRQAPGKLEWVAGINPKNGTSH 60
DB 1 QIQQQSGPELVRPGASVKISCKASGYFTDYIHWVKQRPGEGLWIGWIYPGSGNTKY 60
QY 61 NORFMDRFTISVDKSTSTAYMQMNSLRADTAIVYCARWGLNYGDFVYFVWVGQGLTV 120
DB 61 NEKEFGKATLTVDTSSTAYMQLSLTSEDSAVFYCA--RGKKFA----MDYWGQGTSV 113
QY 121 TVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV 180
DB 114 TVSSAKTAPSVYPLAPVCGDGTGSSVTLGCLVKGYFPEPVTLTWNSSLSGSGVHTFPAV 173
QY 181 LQSSGLYSLSSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKVEPK 225
DB 174 LQSD-LYTLSSSVTVTPSSVQSTTCNVAHPASSTKVDKKIEPR 217

RESULT 5
S40295
Ig gamma-2a chain (mAb735) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 16-Jul-1999
C:Accession: S40295
R:Kiebert, S.; Kratzin, H.D.; Zimmermann, B.; Vaesen, M.; Frosch, M.; Weisgerber, C.;
submitted to the EMBL Data Library, January 1993
A:Description: Primary structure of the murine monoclonal IgG2a antibody mAb735 again
A:Reference number: S40295
A:Accession: S40295
A:Molecule type: protein
A:Residues: 1-446 <KLE>
C:Genetics:
A:Map position: 12
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: disulfide bond; glycoprotein; immunoglobulin; pyroglutamic acid
F:1-446/Product: Ig gamma-2a chain #status experimental <MAT>
F:1-117/Domain: V-D-J region <VDJ>
F:118-446/Domain: C region <CHR>
F:118-214/Domain: C1 region <CH1>
F:215-230/Region: hinge
F:231-340/Domain: C2 region <CH2>
F:341-446/Domain: C3 region <CH3>
F:360-427/Domain: immunoglobulin homology <IMM>
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:22-96,144-199,261-321,367-425/Disulfide bonds: #status predicted
F:132/Disulfide bonds: interchain (to light chain) #status predicted
F:224,227,229/Disulfide bonds: interchain #status predicted
F:297/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 55.8%; Score 688; DB 2; Length 446;


```
Best Local Similarity 57.8%; Pred. No. 1.2e-40;
Matches 130; Conservative 41; Mismatches 46; Indels 8; Gaps 3;

Qy 1 EVLVESGGLVOPGSLRLSCATSGYTFEYTHMWRQAPGKLEWAGINPKNGTSH 60
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1 QIQLQQSGPELVPRGASVKISKASGYTFDYIHWKVRPGEGLEWIGWYPCSGNTKY 60

Qy 61 NQRFMDRFTISVDKSTSTAYMQNSLRAEDTAVYYCARWRGLNGYFDVWVGQGLV 120
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
61 NKFKGKATLTVDTSSTAYMQLSSLTSEDYVYFCARNGA-----MDYWGQGTSV 113

Qy 121 TVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSVGHVTPPAV 180
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
114 TVSSAKTTPSYVPLAPVCGDTGSSVTLGCLVKGVFPEPTVLTWNSGSLSSGVHTTTPAV 173

Qy 181 LOSGLYSLSSVVTVPSSSLGTQTYICNVNHPKSTNTKVDKKVEPK 225
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
174 LQSD-LYTLSSSVTTSWPSQSITCNVAHPASSTKVDKKIEPR 217

RESULT 6
Ig gamma-2a chain - mouse
C:Species: Mus musculus (house mouse)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S37483
R:Ducancel, F.F.D.
submitted to the EMBL Data Library, February 1993
A:Reference number: S37483
A:Accession: S37483
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-469 <DUC>
A:Cross-references: EMBL:X70423; NID:g406252; PIDN:CAA49868.1; PID:g406253
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
F:276-345/Domain: immunoglobulin homology <IMM>

Query Match 55.4%; Score 683.5; DB 2; Length 469;
Best Local Similarity 56.9%; Pred. No. 2.6e-40;
Matches 128; Conservative 41; Mismatches 51; Indels 5; Gaps 2;

Qy 1 EVLVESGGLVOPGSLRLSCATSGYTFEYTHMWRQAPGKLEWAGINPKNGTSH 60
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
20 QIQLQQSGPELVPRGASVKISKASGYTFDYIHWKVRPGEGLEWIGWYPCSGNTKY 79

Qy 61 NQRFMDRFTISVDKSTSTAYMQNSLRAEDTAVYYCARWRGLNGYFDVWVGQGLV 120
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
80 NKFKGKATLTVDTSSTAYMQLSSLTSEDYVYFCARNGAT---ATLLDYWGQGTTL 135

Qy 121 TVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSVGHVTPPAV 180
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
136 TVSSAKTTPSYVPLAPVCGDTGSSVTLGCLVKGVFPEPTVLTWNSGSLSSGVHTTTPAV 195

Qy 181 LOSGLYSLSSVVTVPSSSLGTQTYICNVNHPKSTNTKVDKKVEPK 225
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
196 LQSD-LYTLSSSVTTSWPSQSITCNVAHPASSTKVDKKIEPR 239

RESULT 7
Ig heavy chain (Mab13-1) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 29-Jul-1997 #sequence_revision 29-Aug-1997 #text_change 20-Jun-2000
C:Accession: S68211
R:Tagaki, M.; Kohda, K.; Hamuro, T.; Harada, A.; Yamaguchi, H.; Kamachi, M.;
FEBS Lett. 375, 273-276, 1995
A:Title: Thermostable peroxidase activity with a recombinant antibody L chain-porphyrin
A:Reference number: S68211; MUID:96085223
A:Accession: S68211
A>Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
```

```
A:Residues: 1-220 <TAK>
A:Cross-references: EMBL:D29669; NID:g473958; PIDN:BAA06140.1; PID:g473959
A>Note: the sequence of residues 1-4, 213-220 and the corresponding nucleotide sequen
C:Superfamily: immunoglobulin C region; immunoglobulin homology
F:136-200/Domain: immunoglobulin homology <IMM>

Query Match 55.2%; Score 680.5; DB 2; Length 220;
Best Local Similarity 59.9%; Pred. No. 2e-40;
Matches 136; Conservative 24; Mismatches 54; Indels 13; Gaps 4;

Qy 5 VESGGLVOPGSLRLSCATSGYTFEYTHMWRQAPGKLEWAGINPK--NGGTSHNQ 62
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1 LESGGLVPRGNSLKLSCLTSGTFESNTMHLRQPPGKRLEWIAVITVKSNDYGAKEYAE 60

Qy 63 RFMDRFTISVDKSTSTAYMQNSLRAEDTAVYYCAR--WRGLNYGDFVRYFDVWVGQGLV 120
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
61 SVRGFTISRDRSSSVYQLNRLREEDTATVYCCRTPE-----VYAMDCWQGTSTV 112

Qy 121 TVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSVGHVTPPAV 180
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
113 TVSSAKTTPSYVPLAPGSAATNSMVTGLCLVKGVFPEPTVTVWNSGSLSSGVHTTTPAV 172

Qy 181 LOSGLYSLSSVVTVPSSSLGTQTYICNVNHPKSTNTKVDKKVEPKSC 227
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
173 LQSD-LYTLSSSVTVPSTWTFSETVTCNVAHPASSTKVDKKIVPRDC 218

RESULT 8
G2MS11
Ig gamma-2b chain - mouse
C:Species: Mus musculus (house mouse)
C:Date: 31-Mar-1980 #sequence_revision 01-Dec-2000 #text_change 01-Dec-2000
C:Accession: S25057; A26235; A26232; A26233; A53598
R:Fischer, R.; Voss, A.; Niersbach, M.; Munziker, W.; Hirsch, H.J.; Kreuzaler, F.
submitted to the EMBL Data Library, July 1992
A:Description: Production of a Tobacco mosaic virus (TMV) inactivating neotop specifi
A:Reference number: S25057
A:Accession: S25057
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-474 <FIS>
A:Cross-references: EMBL:X67210; NID:g54826; PIDN:CAA47649.1; PID:g54827
R:Yamawaki-Kataoka, Y.; Kataoka, T.; Takahashi, N.; Obata, M.; Honjo, T.
Nature 283, 786-789, 1980
A:Title: Complete nucleotide sequence of immunoglobulin gamma2b chain gene cloned fro
A:Reference number: A02157; MUID:80120716
A:Contents: a allele
A:Accession: A02157
A:Molecule type: DNA
A:Residues: 138-161, 'L', 163-189, 'FP', 193-474 <YAM>
A:Cross-references: GB:J00461
A>Note: the sequence was determined from the germline gene
R:Tucker, P.W.; Marcu, K.B.; Slightom, J.L.; Blattner, F.R.
Science 206, 1299-1303, 1979
A:Title: Structure of the constant and 3' untranslated regions of the murine gamma2b
A:Reference number: A26235; MUID:80081501
A:Contents: MPC 11
A:Accession: A26235
A:Molecule type: mRNA
A:Residues: 138-172, 'P', 174-189, 'FP', 193-376, 'T', 378-474 <TUI>
A>Note: Lys-474 is probably removed posttranslationally
R:Tucker, P.W.; Marcu, K.B.; Newell, N.; Richards, J.; Blattner, F.R.
Science 206, 1303-1306, 1979
A:Title: Sequence of the cloned gene for the constant region of murine gamma2b immuno
A:Reference number: A26232; MUID:80081502
A:Accession: A26232
A:Molecule type: DNA
A:Residues: 138-172, 'P', 174-189, 'FP', 193-376, 'T', 378-474 <TUI>
R:Ollo, R.; Rougeon, F.
Nature 296, 761-763, 1982
A:Title: Mouse immunoglobulin allotypes: post-duplication divergence of gamma2a and g
A:Reference number: A26233; MUID:82173203
```

A;Contents: b allele
A;Accession: A26233
A;Molecule type: DNA
A;Residues: 138-161,'L',163-189,'FP',193-300,'R',302-331,'A',333-437,'DI',440-474 <OLL>
A;Cross-references: GB:J00461
R;Kim, H.; Yamaguchi, Y.; Masuda, K.; Matsunaga, C.; Yamamoto, K.; Irimura, T.; Takahashi, J. Biol. Chem. 269, 12345-12350, 1994
A;Title: O-glycosylation in hinge region of mouse immunoglobulin G2b.
A;Reference number: A53598; MUID:94216359
A;Accession: A53598
A;Status: preliminary
A;Molecule type: protein
A;Residues: 234-251 <IM>
C;Comment: The a allele sequence is shown.
C;Genetics:
A;Introns: 138/1, 236/1, 258/1, 368/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger disulfide bonds.
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglobulin F;157-222/Domain: immunoglobulin homology <IM1>
F;236-257/Region: hinge
F;281-350/Domain: immunoglobulin homology <IM2>
F;387-454/Domain: immunoglobulin homology <IM3>
F;152/Disulfide bonds: interchain (to light chain) #status predicted
F;164-220,288-348,394-452/Disulfide bonds: #status predicted
F;247,250,253,256/Disulfide bonds: interchain (to heavy chain) #status predicted
F;324/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 54.4%; Score 670.5; DB 1; Length 474;
Best Local Similarity 53.3%; Pred. No. 2.1e-39;
Matches 129; Conservative 37; Mismatches 57; Indels 19; Gaps 3;

QY 1 EVQLVESGGGLVQPGGSLRLSCATSGYTFEYTHMHWRAQPGKLEWVAGINPKNGFTSH 60
Db 20 EVQLQSGPELVAPGASVKMSCKASGTFITYVMHWKQKPGQGLEWIGYINPNKNGTKF 79

QY 61 NORFMDRFTISVDKSTSTAYMQMNSLRAEDTAVYYCARWGLNYGFDVRYFDVMQGQTLV 120
Db 80 NERFKGKATLTSKSSNTAYMELSSLTSEDSAVYYCAR---DYDYD--WFAYWGQGTLLV 133

QY 121 TVSSASTKGPSVFPPLAPSSKSTSGTAAALGCLVKDYFPEPTVTVSNWNSGALTSGVHTFPAP 180
Db 134 TVSAAKTTPPSVYPLAPGCGDTTSGSVTSGCLVKGYFPESVTVTVNWSGSLSSVHTLSQA 193

QY 181 LOSGLYSLSSVTVPPSSSLGTQTYICNVNHPKNTKVDKKVEP-----KSC 227
Db 194 LLOSGLYTMSSSVTVPPSSVTPSQVTCTCSVAHPASSTTVTDKKLEPSPGISTINPCPKCEK 253

QY 228 DK 229
Db 254 HK 255

RESULT 9
S68213
Ig heavy chain (Mab03-1) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 29-Jul-1997 #sequence_revision 17-Sep-1997 #text_change 21-Jan-2000
C;Accession: S68213
R;Takagi, M.; Kohda, K.; Hamuro, T.; Harada, A.; Yamaguchi, H.; Kamachi, M.; Imanaka, T.; FBS Lett. 375, 273-276, 1995
A;Title: Thermostable peroxidase activity with a recombinant antibody L chain-porphyrin
A;Reference number: S68211; MUID:96085223
A;Accession: S68213
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-213 <TAK>
A;Cross-references: EMBL:D29667
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;137-201/Domain: immunoglobulin homology <IM>

Query Match 53.9%; Score 665; DB 2; Length 213;
Best Local Similarity 60.2%; Pred. No. 2.3e-39;
Matches 133; Conservative 28; Mismatches 50; Indels 10; Gaps 3;

QY 2 VOLVESGGGLVQPGGSLRLSCATSGYTFEYTHMHWRAQPGKLEWVAGINPKNGTSHN 61
Db 2 VOLVESGGGLVQPGGSRKLSCAASGFTFSFGMHVWRQAPKEKLEWVAYISSGSSIIYYA 61

QY 62 QRFMDRFTISVDKSTSTAYMQMNSLRAEDTAVYYCAR--WRGLNYGFDVRYFDVMQGQTLV 120
Db 62 DTVKGRFTISRDNPKNTLFLQMTSLRSEDATAMYYCARSW-----LLPFDYWGQGTLL 113

QY 121 TVSSASTKGPSVFPPLAPSSKSTSGTAAALGCLVKDYFPEPTVTVSNWNSGALTSGVHTFPAP 180
Db 114 TVSSAKTTPPSVYPLAPGCGDTTSGSVTLGCLVKGYFPESVTVTVNWSGSLSSVHTFPAL 173

QY 181 LOSGLYSLSSVTVPPSSSLGTQTYICNVNHPKNTKVDKK 221
Db 174 LQ-SGLYTMSSSVTVPPSSVTPSQVTCTCSVAHPASSTTVDDKK 213

RESULT 10
S38864
Ig epsilon chain C region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 24-May-2001
C;Accession: S38864
R;Kipp, B.; Becker, W.; Schlaak, M.
submitted to the EMBL Data Library, November 1993
A;Description: Combination of a defined specificity and desired isotype by cloning of
A;Reference number: S38864
A;Accession: S38864
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-548 <KIP>
A;Cross-references: EMBL:227397; NID:9416537; PID:CAA81788.1; PID:940782
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;353-421/Domain: immunoglobulin homology <IM>

Query Match 53.9%; Score 664.5; DB 2; Length 548;
Best Local Similarity 58.6%; Pred. No. 6.4e-39;
Matches 133; Conservative 34; Mismatches 55; Indels 5; Gaps 3;

QY 1 EVQLVESGGGLVQPGGSLRLSCATSGYTFEYTHMHWRAQPGKLEWVAGINPKNGTSH 60
Db 1 QVKLESGLDLVKPGGSLKLSCAASGLTFSYGMWVRQIPDKRLEWVATISSGGTYIYY 60

QY 61 NORFMDRFTISVDKSTSTAYMQMNSLRAEDTAVYYCARWGLNYGFDVRYFDVMQGQTLV 120
Db 61 PDSVKGRFTISRDNKNTLYLQMSLSKSEDATAMYYCAR--QGVSV---TMRFAYWGQGTLLV 116

QY 121 TVSSASTKGPSVFPPLAPSSKSTSGTAAALGCLVKDYFPEPTVTVSNWNSGALTSGVHTFPAP 180
Db 117 TVSAGKTTTPPSVYPLAPGSAAGTNSMVTLGCLVKGYFPPEPTVTVNWSGSLSSVHTFPAP 176

QY 181 LOSGLYSLSSVTVPPSSSLGTQTYICNVNHPKNTKVDKKVEPKSC 227
Db 177 LQSD-LYTLSSSVTVPPSSVTPSQVTCTCNVAHPASSTKVDKKIVPRDC 222

RESULT 11
PC4202
monoclonal antibody Maba34 gamma1 heavy chain - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1996 #sequence_revision 31-Dec-1996 #text_change 21-Jan-2000
C;Accession: PC4202
R;Kwak, J.W.; Lee, D.I.; Choi, B.K.; Cho, W.K.; Lee, S.H.; Park, Y.B.; Han, M.H.
Gene 173, 257-259, 1996
A;Title: Cloning and characterization of cDNAs coding for heavy and light chains of a
A;Reference number: PC4202; MUID:97082978
A;Accession: PC4202

A:Molecule type: mRNA

A:Residues: 1-214 <KWA>
A:Cross-references: GB:U29146; NID:g1594223; PIDN:AAC52820.1; PID:g1594224
C:Comment: This protein is specific for human plasma apolipoprotein A-I of high-density
C:Superfamily: immunoglobulin C region; immunoglobulin homology
F:1-112/Domain: V region #status predicted <VRG>
F:113-214/Domain: C region #status predicted <CRG>
F:132-196/Domain: immunoglobulin homology <IMM>

Query Match 53.7%; Score 662.5; DB 2; Length 214;
Best Local Similarity 55.5%; Pred. No. 3.4e-39;
Matches 126; Conservative 36; Mismatches 52; Indels 13; Gaps 2;

QY 1 EVLVESGGGLVOPGGSLRLSCATSGYTFEYTMHMRQAPKGLFWAGINPKNGTSH 60
DB 1 EVLVESGAELMKPGASVKISKATDYRESSWIEVKQRPGLGEMIGDILPGSGNTNY 60
QY 61 NORFMDRTTISVDKSTSTAYMQMNSLRADTAVYYCARWRGLNYGFDVRYFDVWGQGTLLV 120
DB 61 NERFKGKATFTADTSSNTAYMQLSLTSEDSAVYYCA-----IPDYWGQGTLL 108
QY 121 TVSSASTKGPSVFPPLAPSKSTSGGTAALGCLVKDYFPEPTVSNWNGALTSGVHTFP 180
DB 109 TVSSAKTTPPSVYPLAPGSAQTNSMVTLGCLVKGYFPEPTVSNWNGSLSSGVHTFP 168
QY 181 LOSGLYSLSSVTVPPSSSLGTQTYICNVNHPKSNTKVDKVEPKSC 227
DB 169 LQSD-LYTLSSSVTVPPSRPSETVTCNVHPASSTKVDKIVPRDC 214

RESULT 12

S49220
Ig gamma-1 chain - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 19-Mar-1997 #sequence_revision 01-Aug-1997 #text_change 21-Jan-2000
C:Accession: S49220
R:Kipp, B.; Becker, W.P.; Schlaak, M.M.
submitted to the EMBL Data Library, September 1994
A:Description: Cloning and expression of a recombinant mouse Fab-fragment recognizing a
A:Reference number: S49220
A:Accession: S49220
A:Molecule type: mRNA
A:Residues: 1-221 <KIP>
A:Cross-references: EMBL:237502; NID:g541778; PIDN:CAA85732.1; PID:g541779
A:Experimental source: strain Balb/c
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
F:1-120/Domain: V region #status predicted <VRG>
F:121-221/Domain: C region #status predicted <CRG>
F:139-203/Domain: immunoglobulin homology <IMM>

Query Match 52.8%; Score 651; DB 2; Length 221;
Best Local Similarity 55.9%; Pred. No. 2.2e-38;
Matches 127; Conservative 37; Mismatches 57; Indels 6; Gaps 4;

QY 1 EVLVESGGGLVOPGGSLRLSCATSGYTFEYTMHMRQAPKGLFWAGINPKNGTSH 60
DB 1 QVKLESAGELVKASGASVKLSCTASGFNPKDYMHVVKQRPGLGEMIGRIDPANGEIKY 60
QY 61 NORFMDRTTISVDKSTSTAYMQMNSLRADTAVYYCARWRGLNYGFDVRYFDVWGQGTLLV 120
DB 61 DPKFGQTATITADTSTNTAYLQSLTSEDTAVYYCVR-RG--YGSSQEPY--WGQGTLL 115
QY 121 TVSSASTKGPSVFPPLAPSKSTSGGTAALGCLVKDYFPEPTVSNWNGALTSGVHTFP 180
DB 116 TVSSAKTTPPSVYPLAPGSAQTNSMVTLGCLVKGYFPEPTVSNWNGSLSSGVHTFP 175
QY 181 LOSGLYSLSSVTVPPSSSLGTQTYICNVNHPKSNTKVDKVEPKSC 227
DB 176 LQSD-LYTLSSSVTVPPSSWPSETVTCNVHPASSTKVDKIVPRDC 221

RESULT 13

S01321
Ig gamma-2b chain precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 23-Jul-1999
C:Accession: S01321
R:de Waele, P.; Feys, V.; van de Voorde, A.; Molemans, F.; Fiers, W.
Eur. J. Biochem. 176, 287-295, 1988
A:Title: Expression in non-lymphoid cells of mouse recombinant immunoglobulin directed
A:Reference number: S01320; MUID:88329081
A:Accession: S01321
A:Molecule type: mRNA
A:Residues: 1-475 <DR1>
A:Cross-references: EMBL:X13188; NID:g51780; PIDN:CAA31580.1; PID:g51781
A:Note: This sequence was determined from the differentiated gene
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-475/Product: Ig gamma-2b chain #status predicted <MAT>
F:159-223/Domain: immunoglobulin homology <IMM>

Query Match 51.5%; Score 635; DB 2; Length 475;
Best Local Similarity 51.7%; Pred. No. 6.2e-37;
Matches 125; Conservative 41; Mismatches 58; Indels 18; Gaps 3;

QY 1 EVLVESGGGLVOPGGSLRLSCATSGYTFEYTMHMRQAPKGLFWAGINPKNGTSH 60
DB 20 QVQLQQSGAELARPGASVKLSKASGYTLTSGYISWVKORTQGLEWIGEIVPGSGNSYF 79
QY 61 NORFMDRTTISVDKSTSTAYMQMNSLRADTAVYYCARWRGLNYGFDVRYFDVWGQGTLLV 120
DB 80 NEKEFKGKATLTVDKSSSTAYLHLSLTSEDSAVYFCAPRQVG-----LLPFGYWGQGTLLV 135
QY 121 TVSSASTKGPSVFPPLAPSKSTSGGTAALGCLVKDYFPEPTVSNWNGALTSGVHTFP 180
DB 136 TASAATTPPSVYPLAPGCGDTTGGSSVTGLGCLVKGYFPEPTVSNWNGSLSSGVHTFP 195
QY 181 LOSGLYSLSSVTVPPSSSLGTQTYICNVNHPKSNTKVDKVEPK-----KSC 227
DB 196 LQ-SGLYTMSSVTVPPSSVTPQVTCVAHPASSTTVDDKLEPSGPTSTINPCPPCKEC 254
QY 228 DK 229
DB 255 HK 256

RESULT 14

PC4155
Ig gamma-2b chain V-C region MabB23 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 10-May-1996 #sequence_revision 19-Jul-1996 #text_change 21-Jan-2000
C:Accession: PC4155
R:Kwak, J.W.; Choi, B.K.; Lee, D.I.; Kang, Y.K.; Seo, Y.G.; Cho, W.K.; Han, M.H.
Gene 189, 237-239, 1996
A:Title: Cloning and characterization of cDNAs coding for heavy and light chains of a
A:Reference number: PC4155; MUID:96194809
A:Accession: PC4155
A:Molecule type: mRNA
A:Residues: 1-231 <KWA>
A:Cross-references: GB:U28970; NID:g1262180; PIDN:AAC52489.1; PID:g1262181
A:Note: This protein has unusual amino acid compared with the conserved sequences of
C:Superfamily: immunoglobulin C region; immunoglobulin homology
F:1-231/Product: heavy chain #status predicted <MAT>
F:98-102/Region: unique D sequence
F:103-119/Region: V region
F:139-203/Domain: immunoglobulin homology <IMM>

Query Match 51.1%; Score 630; DB 2; Length 231;
Best Local Similarity 54.3%; Pred. No. 6.6e-37;
Matches 125; Conservative 32; Mismatches 55; Indels 18; Gaps 4;

Search completed: August 14, 2002, 11:05:26
Job time: 361 sec

```
QY 1 EVQLVESGGGLVQPGGSLRLSVCATSGYTFTEYTHMMWQAPCKGLEWVAGINPKNGGTS 60
      |||||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||
Db 1 EVQLVESGGGLVQPGGSLRLSVCATSGYTFTEYTHMMWQAPCKGLEWVAGINPKNGGTS 59
      |||||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||
QY 61 NQRFMDRFTISVDKSTSTAYMQMNSLRADTAHYICAR-----WRGLNYGDFDYFDWM 114
      |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db 60 NSALKSRSLINKNSKQVFLKMNLSLTDATYICVHEDRYD-----YFDWM 109
      |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
QY 115 GQGLTVTVSSASTKGPSVFLAPSSKSTSGGTAALGCLVLDYFPEPTVTVSNNSGALTSGV 174
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 110 GAGTTVTSSAKTPPSPYIPLAPRCGDTGSSVTLGCLVKGYPFESVTVTWNSGSLSSV 169
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 175 HTPFAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKPSNTKVDKKEP 224
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 170 HTPFALLQ-SGLYTMSSSVTVPSSTWPSQTVCVAHPASSTTVTDKLEP 218
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

RESULT 15
S22080
Ig heavy chain precursor (B/MT.4A.17.H5.A5) - bovine
N:Alternate names: Ig gamma-1 chain C region (clone 8.10)
C:Species: Bos primigenius taurus (cattle)
C:Date: 06-Jan-1995 #sequence-revision 06-Jan-1995 #text-change 23-Jul-1999
C:Accession: S22080; S06610; A31303
R:Sanders, P.G.
submitted to the EMBL Data Library, November 1991
A:Reference number: S22080
A:Accession: S22080
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-470 <SAN>
A:Cross-references: EMBL:X62916; NID:g439; PIDN:CAA44699.1; PID:g440
R:Symons, D.B.A.; Clarkson, C.A.; Beale, D.
Mol. Immunol. 26, 841-850, 1989
A:Title: Structure of bovine immunoglobulin constant region heavy chain gamma 1 and gamma 2
A:Reference number: S06610; MUID:90097956
A:Accession: S06610
A:Molecule type: DNA
A:Residues: 142-470 <SYM>
A:Cross-references: EMBL:X16701
A>Note: the sequence was determined from the germline gene
C:Genetics:
A:Gene: Ig CH gamma-1
A:Introns: 98/1; 111/1; 221/1
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: glycoprotein; heterotetramer; immunoglobulin; membrane protein
F:161-225/Domain: immunoglobulin homology <IMM>
F:318/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 49.8%; Score 614.5; DB 2; Length 470;
Best Local Similarity 54.9%; Pred. No. 1.6e-35;
Matches 129; Conservative 27; Mismatches 66; Indels 13; Gaps 6;

QY 1 EVQLVESGGGLVQPGGSLRLSVCATSGYTFTEYTHMMWQAPCKGLEWVAGINPKNGGTS- 59
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 20 QVQLRESGPSLVKPSQTLSTCTVSGFSLSSYALTWVRQAPGKALEWVGIT--SGGTTY 77
      |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
QY 60 HNQRMDRFTISVDKSTSTAYMQMNSLRADTAHYICARWGLNYG--FDVRYFDWVGQ 117
      |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db 78 YNPALKSRSLITKENSQVSLSVSTPDTATYICAR---STYGEVGDGAIDAWGQ 134
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 118 TLTVTVSSASTKGPSVFLAPSSKSTSGTAAALGCLVLDYFPEPTVTVSNNSGALTSGVHTF 177
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 135 LLTVTVSSASTAPKVPFLSSCCCGKSSSTVTGLCLVSSYMPPEPTVTWNSGALKSGVHTF 194
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 178 PAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKPSNTKVDKKEV----PKSCD 228
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 195 PAVLQSSGLYSLSSMTVPGSTG-QTFCTCNVHPASSTKVDKAYDPTCKPSPCD 248
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
```

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 14, 2002, 11:01:15 ; Search time 16.05 Seconds
(without alignments)
559.684 Million cell updates/sec

Title: US-09-811-384-10

Perfect score: 1233

Sequence: 1 EVQVSGGGLVPGGSLRL.....PSNTKVDKVKPKSCDKTHT 232

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	563	45.7	330	1	GCL_HUMAN
2	475	38.5	326	1	G22_HUMAN
3	474	38.4	327	1	G24_HUMAN
4	416	33.7	120	1	HV50_MOUSE
5	405.5	32.9	117	1	HV12_MOUSE
6	405.5	32.9	117	1	HV13_MOUSE
7	399	32.4	122	1	HV3G_HUMAN
8	395	32.0	118	1	HV51_MOUSE
9	392	31.8	137	1	HV11_MOUSE
10	392	31.8	139	1	HV07_MOUSE
11	391	31.7	122	1	HV21_MOUSE
12	384	31.1	122	1	HV20_MOUSE
13	382	31.0	119	1	HV38_MOUSE
14	380.5	30.9	115	1	HV3D_HUMAN
15	380.5	30.9	123	1	HV18_MOUSE
16	379.5	30.8	123	1	HV19_MOUSE
17	379.5	30.8	123	1	HV25_MOUSE
18	377.5	30.6	117	1	HV17_MOUSE
19	377.5	30.6	123	1	HV23_MOUSE
20	376.5	30.5	121	1	HV33_MOUSE
21	375.5	30.5	123	1	HV22_MOUSE
22	374.5	30.4	119	1	HV31_HUMAN
23	373.5	30.3	142	1	HV01_RAT
24	371	30.1	136	1	HV16_MOUSE
25	370	30.0	119	1	HV37_MOUSE
26	369.5	30.0	120	1	HV03_MOUSE
27	369	29.9	119	1	HV40_MOUSE
28	369	29.9	120	1	HV30_HUMAN
29	368.5	29.9	123	1	HV24_MOUSE
30	367.5	29.8	120	1	HV3E_HUMAN
31	367.5	29.8	144	1	HV26_MOUSE
32	365	29.6	114	1	HV01_CANFA
33	365	29.6	147	1	HV1C_HUMAN

ALIGNMENTS

RESULT 1	GCL_HUMAN	117	1	HV3C_HUMAN	P01764	homo sapien
ID	GCL_HUMAN	STANDARD;	PRT;	330 AA.		
AC	P01857;					
DT	21-JUL-1986 (Rel. 01, Created)					
DT	21-JUL-1986 (Rel. 01, Last sequence update)					
DT	16-OCT-2001 (Rel. 40, Last annotation update)					
DE	Ig gamma-1 chain C region.					
GN	IGHG1.					
OS	Homo sapiens (Human).					
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
OX	NCBI_TaxID=9606;					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RX	MEDLINE=82274238; PubMed=6287432;					
RA	Ellison J.W., Berson B.J., Hood L.E.;					
RT	"The nucleotide sequence of a human immunoglobulin C gamma1 gene."					
RL	Nucleic Acids Res. 10:4071-4079(1982).					
RN	[2]					
RP	SEQUENCE OF 1-135 (MYELOMA PROTEIN EU).					
RX	MEDLINE=71064024; PubMed=5489771;					
RA	Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,					
RT	Waxdal M.J., Edelman G.M.;					
RT	"The covalent structure of a human gamma G-immunoglobulin. VII. Amino					
RL	acid sequence of heavy-chain cyanogen bromide fragments H1-H4."					
RL	Biochemistry 9:3161-3170(1970).					
RN	[3]					
RP	SEQUENCE OF 136-329 (EU).					
RX	MEDLINE=71064025; PubMed=5530842;					
RA	Rutishauser U., Cunningham B.A., Bennett C., Konigsberg W.H.,					
RT	Edelman G.M.;					
RT	"The covalent structure of a human gamma G-immunoglobulin. 8. Amino					
RL	acid sequence of heavy-chain cyanogen bromide fragments H5-H7."					
RL	Biochemistry 9:3171-3181(1970).					
RN	[4]					
RP	SEQUENCE (MYELOMA PROTEIN NIE).					
RX	MEDLINE=77070269; PubMed=826475;					
RA	Ponstingl H., Hilschmann N.;					
RT	"The rule of antibody structure. The primary structure of a					
RT	monoclonal IgG1 immunoglobulin (myeloma protein NIE). III. The					
RT	chymotryptic peptides of the H-chain, alignment of the tryptic					
RL	peptides and discussion of the complete structure."					
RL	Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).					
RN	[5]					
RP	SEQUENCE (MYELOMA PROTEIN KOL), AND DISULFIDE BONDS.					
RX	MEDLINE=83289131; PubMed=688494;					
RA	Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;					
RT	"Three-dimensional structure determination of antibodies. Primary					
RT	structure of crystallized monoclonal immunoglobulin IgG1 KOL, I."					
RT	Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).					
RN	[6]					
RP	DISULFIDE BONDS.					
RX	MEDLINE=71064027; PubMed=4923144;					
RA	Gall W.E., Edelman G.M.;					
RT	"The covalent structure of a human gamma G-immunoglobulin. X.					

34	363	29.4	117	1	HV3C_HUMAN	P01764	homo sapien
35	363	29.4	122	1	HV3H_HUMAN	P01769	homo sapien
36	361.5	29.3	140	1	HV02_MOUSE	P01746	mus musculus
37	361	29.3	117	1	HV3T_HUMAN	P01776	homo sapien
38	359	29.1	116	1	HV30_HUMAN	P01781	homo sapien
39	358.5	29.1	118	1	HV39_MOUSE	P01809	mus musculus
40	357.5	29.0	138	1	HV48_MOUSE	P03980	mus musculus
41	357	29.0	114	1	HV3B_HUMAN	P01763	homo sapien
42	356.5	28.9	115	1	HV3F_HUMAN	P01767	homo sapien
43	352.5	28.6	117	1	HV41_MOUSE	P01811	mus musculus
44	351.5	28.5	113	1	HV30_MOUSE	P01799	mus musculus
45	351.5	28.5	115	1	HV32_MOUSE	P01801	mus musculus

[3] SEQUENCE OF 99-177 AND 310-326 FROM N.A.
 RP TISSUE-Fetal liver;
 RC MEDLINE=84235992; PubMed=6329676;
 RA Krawinkel U., Rabbitts T.H.;
 RT "Comparison of the hinge-coding segments in human immunoglobulin gamma
 heavy chain genes and the linkage of the gamma 2 and gamma 4 subclass
 genes.";
 RL EMBO J. 1:403-407(1982).
 RN [4]
 RP SEQUENCE OF 1-325 (MYELOMA PROTEIN TIL).
 RX MEDLINE=81007873; PubMed=6774012;
 RA Wang A.-C., Tung E., Fudenberg H.H.;
 RT "The primary structure of a human IgG2 heavy chain: genetic,
 evolutionary, and functional implications.";
 RL J. Immunol. 125:1048-1054(1980).
 RN [5]
 RP SEQUENCE OF 1-85 AND 132-325 (MYELOMA PROTEIN ZIE).
 RX MEDLINE=80001357; PubMed=113060;
 RA Connell G.E., Parr D.M., Hofmann T.;
 RT "The amino acid sequences of the three heavy chain constant region
 domains of a human IgG2 myeloma protein.";
 RL Can. J. Biochem. 57:758-767(1979).
 RN [6]
 RP SEQUENCE OF 238-275 (ZIE).
 RX MEDLINE=80114419; PubMed=118920;
 RA Hofmann T., Parr D.M.;
 RT "A note of the amino acid sequence of residues 381-391 of human
 immunoglobulins gamma chains.";
 RL Mol. Immunol. 16:923-925(1979).
 RN [7]
 RP REVISIONS TO 25; 59; 60 AND 264-268 (ZIE).
 RA Hofmann T., Parr D.M.;
 RT Submitted (MAR-1980) to the PIR data bank.
 RN [8]
 RP SEQUENCE OF 1-121 (DOT).
 RX MEDLINE=9525298; PubMed=7737190;
 RA Stoppini M., Bellotti V., Negri A., Merlini G., Garver F., Ferri G.;
 RT "Characterization of the two unique human anti-flavin monoclonal
 immunoglobulins.";
 RL Eur. J. Biochem. 228:886-893(1995).
 RN [9]
 RP DISULFIDE BONDS.
 RX MEDLINE=72033500; PubMed=4940472;
 RA Milstein C., Frangione B.;
 RT "Disulphide bridges of the heavy chain of human immunoglobulin G2.";
 RL Biochem. J. 121:217-225(1971).
 RN [10]
 RP DISULFIDE BONDS.
 RX MEDLINE=69064124; PubMed=5782707;
 RA Frangione B., Milstein C., Pink J.R.L.;
 RT "Structural studies of immunoglobulin G.";
 RL Nature 221:145-148(1969).
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; J00230; AAB59393.1; -
 DR PIR; A02148; G2HU.
 DR HSSP; P01857; 1FC1.
 DR MIM; 147110; -
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003597; Ig_cl.
 DR InterPro; IPR003600; Ig_like.
 DR Pfam; PF00047; Ig; 3.
 DR SMART; SM00410; Ig_Like; 1.
 DR SMART; SM00407; IGcl; 2.
 DR PROSITE; PS00290; IG_MHC; 2.

KW Immunoglobulin domain; Immunoglobulin C region.
 FT NON_TER 1 1
 FT DOMAIN 1 98 CHI.
 FT DOMAIN 99 110 HINGE.
 FT DOMAIN 111 219 CH2.
 FT DOMAIN 220 326 CH3.
 FT DISULFID 14 14 INTERCHAIN (WITH A LIGHT CHAIN).
 FT DISULFID 27 83
 FT DISULFID 102 102 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 103 103 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 140 200
 FT DISULFID 246 304
 FT SITE 156 156
 FT MOD_RES 326 326
 FT VARIANT 60 60
 FT CONFLICT 109 109
 FT SEQUENCE 326 AA; 35884 MW; 8310878C6878CF9C CRC64;
 SQ
 Query Match 38.5%; Score 475; DB 1; Length 326;
 Best Local Similarity 89.3%; Pred. No. 7e-34;
 Matches 92; Conservative 3; Mismatches 8; Indels 0; Gaps 0;
 QY 125 ASTKGPSVFLAPSKSTSGTAAALGCLVKDYFPPEVTVSWNSGALTSGVHTFFAVLOSS 184
 DB 1 ASTKGPSVFLAPSKSTSGTAAALGCLVKDYFPPEVTVSWNSGALTSGVHTFFAVLOSS 60
 QY 185 GLYSLSSVTVPPSSSLGTQTYICNVNHPKSNKTKVDKVKPKSC 227
 DB 61 GLYSLSSVTVPPSSSLGTQTYICNVNHPKSNKTKVDKTKVERKCC 103
 RESULT 3
 GC4_HUMAN
 ID GC4_HUMAN STANDARD; PRT; 327 AA.
 AC P01861;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DE 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Ig gamma-4 chain C region.
 GN IGHG4.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=83157104; PubMed=6299662;
 RA Ellison J.W., Buxbaum J.N., Hood L.E.;
 RT "Nucleotide sequence of a human immunoglobulin C gamma 4 gene.";
 RL DNA 1:11-18(1981).
 RN [2]
 RP SEQUENCE OF 1-30 AND 81-326.
 RX MEDLINE=70207560; PubMed=4192699;
 RA Pink J.R.L., Buttery S.H., de Vries G.M., Milstein C.;
 RT "Human immunoglobulin subclasses. Partial amino acid sequence of the
 constant region of a gamma 4 chain.";
 RL Biochem. J. 117:33-47(1970).
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; K01316; AAB59394.1; ALT_INIT.
 DR PIR; A02150; G4HU.
 DR HSSP; P01842; 7FAB.

DR MIM: 147130; --
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003597; Ig_c1.
 DR InterPro: IPR003600; Ig_like.
 DR Pfam: PF00047; Ig; 3.
 DR SMART: SM00410; Ig_like; 1.
 DR SMART: SM00407; Ig_c1; 2.
 DR PROSITE: PS00290; IG_MHC; 2.
 KW Immunoglobulin domain; Immunoglobulin C region.
 FT NON_TER 1 98
 FT DOMAIN 1 98 CH1.
 FT DOMAIN 99 110 HINGE.
 FT DOMAIN 111 220 CH2.
 FT DOMAIN 221 327 CH3.
 FT DISULFID 14 14 INTERCHAIN (WITH A LIGHT CHAIN).
 FT DISULFID 27 83 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 141 201
 FT DISULFID 247 305
 SQ SEQUENCE 327 AA; 35940 MW; 3EDBD811EP208E7A CRC64;

Query Match 38.4%; Score 474; DB 1; Length 327;
 Best Local Similarity 91.1%; Pred. No. 8.6e-34;
 Matches 92; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 125 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 184
 Db 1 ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60
 Qy 185 GLYSLSSVTVPPSSSLGTQTYICNVNHPKSNKVDKKEPK 225
 Db 61 GLYSLSSVTVPPSSSLGTQTYICNVNHPKSNKVDKRVESK 101

RESULT 4

ID HV50_MOUSE STANDARD; PRT; 120 AA.
 AC P06329;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-JAN-1988 (Rel. 06, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig heavy chain V region AC38 15.3.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=84182519; PubMed=6201362;
 RA Dildrop R., Bovens J., Siekevitz M., Beyreuther K., Rajewsky K.;
 RT "A V region determinant (idiotope) expressed at high frequency in B
 RT lymphocytes is encoded by a large set of antibody structural genes.";
 RL EMO J. 3:517-523(1984).
 DR PIR; A02037; MHMS15.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_v.
 DR Pfam: PF00047; Ig; 1.
 DR SMART; SM00406; IGv; 1.
 KW Immunoglobulin V region.
 FT DOMAIN 1 98 V SEGMENT.
 FT DOMAIN 99 105 D SEGMENT.
 FT DOMAIN 106 120 J SEGMENT.
 FT DISULFID 22 96 BY SIMILARITY.
 FT NON_TER 120 120
 SQ SEQUENCE 120 AA; 13311 MW; 914453F426F09834 CRC64;

Query Match 33.7%; Score 416; DB 1; Length 120;
 Best Local Similarity 60.5%; Pred. No. 2.6e-29;
 Matches 75; Conservative 22; Mismatches 23; Indels 4; Gaps 2;

Qy 1 EVQLVESGGGLVQPGGSLRLSCATSGYTFETTHWMRQAPGKGLWVAGINPKNGGTS 60
 Db 1 QVQLQPGTELVPKPGASVNLSCASGYTFTSYWMMHWRQAPGKGLWIGGINPSNGGTY 60
 Qy 61 NQREMDRTISVDKSTSTAYMQMNSLRADTAVYYCARWGLNYGFDVRYFDVWGQGLV 120
 Db 61 NEKFKRATLTVDKSSSATYMQLSPTPSDSAVYYCARW---DYEGD-RYFDVWGQGLV 116
 Qy 121 TVSS 124
 Db 117 TVSS 120
 RESULT 5
 HV12_MOUSE STANDARD; PRT; 117 AA.
 ID HV12_MOUSE
 AC P01756;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig heavy chain V region MOPC 104E.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=83075344; PubMed=6816276;
 RA Kehry M.R., Fuhrman J.S., Schilling J.W., Rogers J., Sibley C.H.,
 RA Hood L.E.;
 RT "Complete amino acid sequence of a mouse mu chain: homology among
 RT heavy chain constant region domains.";
 RL Biochemistry 21:5415-5424(1982).
 CC -I- MISCELLANEOUS: THE SEQUENCE OF THE LIGHT CHAIN OF THIS IGM MYELOMA
 CC PROTEIN HAS ALSO BEEN DETERMINED.
 CC -I- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
 DR PIR; A02039; MHMS4E.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_v.
 DR Pfam: PF00047; Ig; 1.
 DR SMART; SM00406; IGv; 1.
 KW Immunoglobulin V region; Glycoprotein.
 FT DISULFID 22 96 BY SIMILARITY.
 FT CARBOHYD 55 55 N-LINKED (GLCNAC. . .).
 FT NON_TER 117 117
 SQ SEQUENCE 117 AA; 12983 MW; 3CF8ACE4BE447E41 CRC64;

Query Match 32.9%; Score 405.5; DB 1; Length 117;
 Best Local Similarity 61.3%; Pred. No. 2e-28;
 Matches 76; Conservative 21; Mismatches 20; Indels 7; Gaps 2;

Qy 1 EVQLVESGGGLVQPGGSLRLSCATSGYTFETTHWMRQAPGKGLWVAGINPKNGGTS 60
 Db 1 EVQLQQSGPELVPKPGASVNMKSCASGYTFTDYMKRWKQSHGKSLWIGDINPNNGGTSY 60
 Qy 61 NQREMDRTISVDKSTSTAYMQMNSLRADTAVYYCARWGLNYGFDVRYFDVWGQGLV 120
 Db 61 NQKFKRATLTVDKSSSATYMQLSLTSDSAVYYCAR----DYDW---YFDVWGQGLV 113
 Qy 121 TVSS 124
 Db 114 TVSS 117
 RESULT 6
 HV13_MOUSE STANDARD; PRT; 117 AA.
 ID HV13_MOUSE
 AC P01757;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig heavy chain V region J558.


```
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=80078170; PubMed=6765983;
RA Schilling J., Clevinger B., Davie J.M., Hood L.;
RT Amino acid sequence of homogeneous antibodies to dextran and DNA
RT rearrangements in heavy chain V-region gene segments.";
RL Nature 283:35-40(1980).
CC -1- MISCELLANEOUS: THE SEQUENCES OF 10 HYBRIDOMA PROTEINS THAT ALSO
CC BIND DEXTRAN DIFFER FROM THAT SHOWN AT 1-7 POSITIONS, MANY OF
CC WHICH OCCUR IN THE D AND J SEGMENTS.
CC -1- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
DR PIR; A26242; MHMSJ5.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
KW Immunoglobulin V region.
FT DISULFID 22 96
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 13024 MW; 292E2AF4BE447E41 CRC64;

Query Match 32.9%; Score 405.5; DB 1; Length 117;
Best Local Similarity 59.8%; Pred. No. 2e-28;
Matches 76; Conservative 19; Mismatches 19; Indels 13; Gaps 2;

QY 1 EVQLVESGGGLVQPGGSLRLSCATSGYTFETHTMHWRAQPKGLEWVAGINPKNGTSH 60
Db 1 EVQLQQSGPELVKPGASVKMSCKASGYTFDTYMKWKVQSHGKSLIEWIGDINPNNGTST 60

QY 61 NQRFMDRFTISVDKSTAYMQMNSLRAEDTAVYYCAR---WRGLNYGFDVRYFDVWGOG 117
Db 61 NQKFKGKATLVDKSSSPAYQLNSLTSEDSAVYYCARDRYW-----YFDVWGAG 110

QY 118 TLTVSS 124
Db 111 TTVTVSS 117

RESULT 7
HV3G_HUMAN STANDARD; PRT; 122 AA.
ID HV3G_HUMAN
AC P01768;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V-III region CAM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=81013859; PubMed=6774332;
RA Lehman D.W., Putnam F.W.;
RT Amino acid sequence of the variable region of a human mu chain:
RT location of a possible JH segment.";
RL Proc. Natl. Acad. Sci. U.S.A. 77:3239-3243(1980).
CC -1- MISCELLANEOUS: THIS MU CHAIN WAS ISOLATED FROM THE PLASMA OF A
CC PATIENT WITH MACROGLOBULINEMIA.
DR PIR; A02051; M3HUAM.
DR HSSP; P01772; 2IG2.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
KW Immunoglobulin V region.
FT MOD_RES 1 1
FT NON_TER 122 122
PYRROLIDONE CARBOXYLIC ACID.

Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=80078170; PubMed=6765983;
RA Schilling J., Clevinger B., Davie J.M., Hood L.;
RT Amino acid sequence of homogeneous antibodies to dextran and DNA
RT rearrangements in heavy chain V-region gene segments.";
RL Nature 283:35-40(1980).
CC -1- MISCELLANEOUS: THE SEQUENCES OF 10 HYBRIDOMA PROTEINS THAT ALSO
CC BIND DEXTRAN DIFFER FROM THAT SHOWN AT 1-7 POSITIONS, MANY OF
CC WHICH OCCUR IN THE D AND J SEGMENTS.
CC -1- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
DR PIR; A26242; MHMSJ5.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
KW Immunoglobulin V region.
FT DISULFID 22 96
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 13024 MW; 292E2AF4BE447E41 CRC64;

Query Match 32.9%; Score 405.5; DB 1; Length 117;
Best Local Similarity 59.8%; Pred. No. 2e-28;
Matches 76; Conservative 19; Mismatches 19; Indels 13; Gaps 2;

QY 1 EVQLVESGGGLVQPGGSLRLSCATSGYTFETHTMHWRAQPKGLEWVAGINPKNGTSH 60
Db 1 EVQLQQSGPELVKPGASVKMSCKASGYTFDTYMKWKVQSHGKSLIEWIGDINPNNGTST 60

QY 61 NQRFMDRFTISVDKSTAYMQMNSLRAEDTAVYYCAR---WRGLNYGFDVRYFDVWGOG 117
Db 61 NQKFKGKATLVDKSSSPAYQLNSLTSEDSAVYYCARDRYW-----YFDVWGAG 110

QY 118 TLTVSS 124
Db 111 TTVTVSS 117

RESULT 7
HV3G_HUMAN STANDARD; PRT; 122 AA.
ID HV3G_HUMAN
AC P01768;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V-III region CAM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=81013859; PubMed=6774332;
RA Lehman D.W., Putnam F.W.;
RT Amino acid sequence of the variable region of a human mu chain:
RT location of a possible JH segment.";
RL Proc. Natl. Acad. Sci. U.S.A. 77:3239-3243(1980).
CC -1- MISCELLANEOUS: THIS MU CHAIN WAS ISOLATED FROM THE PLASMA OF A
CC PATIENT WITH MACROGLOBULINEMIA.
DR PIR; A02051; M3HUAM.
DR HSSP; P01772; 2IG2.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
KW Immunoglobulin V region.
FT MOD_RES 1 1
FT NON_TER 122 122
PYRROLIDONE CARBOXYLIC ACID.
```

```
SQ SEQUENCE 122 AA; 13668 MW; A42D0F17D252F1C2 CRC64;

Query Match 32.4%; Score 399; DB 1; Length 122;
Best Local Similarity 64.5%; Pred. No. 7.8e-28;
Matches 80; Conservative 13; Mismatches 29; Indels 2; Gaps 2;

QY 1 EVQLVESGGGLVQPGGSLRLSCATSGYTFETHTMHWRAQPKGLEWVAGINPKNGTSH 60
Db 1 QVELVESGGGVZPGRSLRSLSCASGTFSTNYAMHWVRQPPGKGLWEVAVISYGBBKYY 60

QY 61 NQRFMDRFTISVDKSTAYMQMNSLRAEDTAVYYCARWGLNYGFDVRYFDVWGOGTLV 120
Db 61 ABSVKGFTISRDSEKETHLYQMNSLRAEDTAVYYCARDRL-YG-BYRAFNWVGQGLV 118

QY 121 TVSS 124
Db 119 TVSS 122

RESULT 8
HV5I_MOUSE STANDARD; PRT; 118 AA.
ID HV5I_MOUSE
AC P06330;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region AC38 205.12.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=84182519; PubMed=6201362;
RA Dildrop R., Bovens J., Siekevitz M., Beyreuther K., Rajewsky K.;
RT "A V region determinant (idiotope) expressed at high frequency in B
RT lymphocytes is encoded by a large set of antibody structural genes.";
RL EMBO J. 3:517-523(1984).
DR PIR; A02040; MHMS38.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 98
FT DOMAIN 99 104
FT DOMAIN 105 118
FT DISULFID 22 96
FT NON_TER 118 118
BY SIMILARITY.
SQ SEQUENCE 118 AA; 12934 MW; 94F7BEE4C762A018 CRC64;

Query Match 32.0%; Score 395; DB 1; Length 118;
Best Local Similarity 58.9%; Pred. No. 1.7e-27;
Matches 73; Conservative 22; Mismatches 23; Indels 6; Gaps 2;

QY 1 EVQLVESGGGLVQPGGSLRLSCATSGYTFETHTMHWRAQPKGLEWVAGINPKNGTSH 60
Db 1 EVQLQQSGPELVKPGASVKISCRASGYTFDTYNNWVKQSHGKSLIEWIGDINPNNGTST 60

QY 61 NQRFMDRFTISVDKSTAYMQMNSLRAEDTAVYYCARWGLNYGFDVRYFDVWGOGTLV 120
Db 61 NQKFKGKATLVDKSSATYMLRSLTSEDSAVYYCAR---GYGDP--FDVWGVTGV 114

QY 121 TVSS 124
Db 115 TVSS 118

RESULT 9
HV1I_MOUSE STANDARD; PRT; 137 AA.
ID HV1I_MOUSE
```



```
RT "Structural evidence for independent joining region gene in
RT immunoglobulin heavy chains from anti-galactan myeloma proteins and
RT its potential role in generating diversity in
RT complementarity-determining regions.";
RL Proc. Natl. Acad. Sci. U.S.A. 76:2890-2894 (1979).
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGA MYELOMA PROTEIN
CC THAT BINDS GALACTAN.
DR PIR; A02078; AVMST6.
DR HSSP; P01810; 2FB7.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR Immunoglobulin V region.
KW NON_TER 119
FT SEQUENCE 119 AA; 13169 MW; BC38CC84E6EA00E8 CRC64;

Query Match 31.0%; Score 382; DB 1; Length 119;
Best Local Similarity 58.9%; Pred. No. 2.2e-26;
Matches 73; Conservative 18; Mismatches 27; Indels 6; Gaps 2;

QY 1 EVLVESGGGLVQPGGSLRLSCAASGFTFTYTHMWRQAPGKGLVWVAGINPKNGTSH 60
DB 1 EVKLLEGGGLVQPGGSLRLSCAASGFTSRYWMSVWRQAPGKGLVWVAGINPKNGTSH 60
QY 61 NQRFMDRFTISVDKSTSTAYMQMNSLRAEDTAVYICARWRGLNYGDFVYFDVWGQGTFLV 120
DB 61 TPSLKDKFIISDNKNTLIYQMSKVRSEDYALYCAR---LCY---YGFVWVGAGTTFV 114
QY 121 TVSS 124
DB 115 TVSS 118

RESULT 14
HV3D_HUMAN
ID HV3D_HUMAN STANDARD; PRT; 115 AA.
AC P01765;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V-III region TIL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=78005528; PubMed=409716;
RA Wang A.-C., Wang I.-Y., Fudenberg H.H.;
RT "Immunoglobulin structure and genetics. Identity between variable
RT regions of a mu and a gamma2 chain.";
RL J. Biol. Chem. 252:7192-7199(1977).
CC -!- MISCELLANEOUS: THE SEQUENCES OF THE V REGIONS OF THE HEAVY CHAINS
CC OF IGM AND IGG2 ISOLATED FROM A SINGLE PATIENT WITH BICLONAL
CC GAMMOPATHY ARE IDENTICAL. THEIR LIGHT CHAINS ARE APPARENTLY ALSO
CC IDENTICAL.
DR PIR; A02048; H3HUTL.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR Immunoglobulin V region.
KW NON_TER 115
FT SEQUENCE 115 AA; 12356 MW; 4DCC67D179F62326 CRC64;

Query Match 30.9%; Score 380.5; DB 1; Length 115;
Best Local Similarity 62.1%; Pred. No. 2.9e-26;
Matches 77; Conservative 12; Mismatches 26; Indels 9; Gaps 2;

QY 1 EVLVESGGGLVQPGGSLRLSCATSGYTFTEYTHMWRQAPGKGLVWVAGINPKNGTSH 60
```

```
DB 1 EVOLLEGGGLVQPGGSLRLSCAASGFTFTYVMSWRQAPGKGLZWVGAIZGLSVSZSY 60
QY 61 NQRFMDRFTISVDKSTSTAYMQMNSLRAEDTAVYICARWRGLNYGDFVYFDVWGQGTFLV 120
DB 61 ABSVKGRFTISDRDSSKNT---MNSLRAEDTAVYICARGRVSAI-----YFVWVGZGTLV 111
QY 121 TVSS 124
DB 112 TVSS 115

RESULT 15
HV18_MOUSE
ID HV18_MOUSE STANDARD; PRT; 123 AA.
AC P01757;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V regions TEPC 15/S107/HPCM1/HPCM2/HPCM3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE (TEPC 15).
RX MEDLINE=80199926; PubMed=819932;
RA Rudikoff S., Potter M.;
RT "Size differences among immunoglobulin heavy chains from
RT phosphorylcholine-binding proteins.";
RL Proc. Natl. Acad. Sci. U.S.A. 73:2109-2112(1976).
RN [2]
RP SEQUENCE FROM N.A. (H107).
RX MEDLINE=80199926; PubMed=6769593;
RA Early P., Huang H., Davis M., Calame K., Hood L.;
RT "An immunoglobulin heavy chain variable region gene is generated from
RT three segments of DNA: VH, D and JH.";
RL Cell 19:981-992(1980).
RN [3]
RP SEQUENCE (S107).
RX MEDLINE=76110488; PubMed=813561;
RA Rudikoff S., Barstad P., Potter M., Hood L.;
RT Unpublished results, cited by:
RL Hood L., Campbell J.H., Elgin S.C.R.;
RL Annu. Rev. Genet. 9:305-353(1975).
RN [4]
RP SEQUENCE (HPCM1; HPCM2 AND HPCM3).
RX MEDLINE=81197602; PubMed=7231520;
RA Gearhart P.J., Johnson N.D., Douglas R., Hood L.;
RT "Ig antibodies to phosphorylcholine exhibit more diversity than
RT their IgM counterparts.";
RL Nature 291:29-34(1981).
CC -!- MISCELLANEOUS: ALL THOSE SEQUENCE APPEARS TO BE IDENTICAL.
CC -!- MISCELLANEOUS: THESE CHAINS WERE ISOLATED FROM MYELOMA AND
CC HYBRIDOMA PROTEINS THAT BIND PHOSPHORYLCHOLINE.
DR PIR; A02070; AVMST5.
DR HSSP; P01789; IMCP.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Hybridoma.
FT NON_TER 123
FT SEQUENCE 123 AA; 13777 MW; 9D58086DE12F7000 CRC64;

Query Match 30.9%; Score 380.5; DB 1; Length 123;
Best Local Similarity 61.1%; Pred. No. 3.1e-26;
Matches 77; Conservative 13; Mismatches 31; Indels 5; Gaps 2;

QY 1 EVLVESGGGLVQPGGSLRLSCATSGYTFTEYTHMWRQAPGKGLVWVAGINPKNGS--T 58
DB 1 EVKLLEGGGLVQPGGSLRLSCATSGTFSDFYMEWRQPPGKRLVIAAARNKANDYTT 60
```

```
QY 59 SHNOREMDREFTISVDKSTSTAYMOMNSIARAEDTAVYICARWRGLNYGFDVRYFDVWGOGT 118
Db 61 EYSASVKGREIVSRDTSQSILYLOMNALEAEDTAIYYCAR---DYIGSSYWFYFDVWGAGT 117
QY 119 LVTVSS 124
Db 118 TTVTVSS 123
```

Search completed: August 14, 2002, 11:07:34
Job time: 379 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 14, 2002, 11:00:50 ; Search time 46.4 Seconds
(without alignments)
864.975 Million cell updates/sec

Title: US-09-811-384-10
Perfect score: 1233
Sequence: 1 EVQLVESGGGLVQPGGSLRL.....PSNTKYDKVKPKSCDKTHT 232

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phase.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	743.5	60.3	278	11	Q921K1	Q921k1 mus musculus
2	717.5	58.2	473	11	Q99125	Q99125 mus musculus
3	709	57.5	473	11	Q9D8L4	Q9d8l4 mus musculus
4	693	56.2	473	11	Q91205	Q91205 mus musculus
5	682	55.3	468	11	Q991L31	Q991l31 mus musculus
6	679.5	55.1	463	11	Q991LC4	Q991lc4 mus musculus
7	653.5	53.0	437	11	Q9RIA4	Q9ria4 mus musculus
8	543	44.0	597	4	Q96BB9	Q96bb9 homo sapien
9	508	41.2	494	4	Q96K68	Q96k68 homo sapien
10	501	40.6	614	4	Q96GA6	Q96ga6 homo sapien
11	496.5	40.3	479	11	Q91LWP5	Q91lpw5 mus musculus
12	489	39.7	488	11	Q91LWR1	Q91lwr1 mus musculus
13	478.5	38.8	487	11	Q99KA4	Q99ka4 mus musculus
14	477	38.7	486	11	Q91Z07	Q91z07 mus musculus
15	477	38.7	500	4	Q9BRV0	Q9brv0 homo sapien
16	464	37.6	147	4	Q9Y509	Q9y509 homo sapien

17	464	37.6	484	11	Q99LA6	Q99la6 mus musculus
18	462.5	37.5	481	11	Q91WT1	Q91wt1 mus musculus
19	456.5	37.0	480	11	Q91XE1	Q91xel mus musculus
20	455	36.9	496	4	Q96DK0	Q96dk0 homo sapien
21	445.5	36.1	481	11	Q91WT3	Q91wt3 mus musculus
22	431	35.0	143	11	Q924Q5	Q924q5 mus musculus
23	427.5	34.7	142	11	Q924Q1	Q924q1 mus musculus
24	427.5	34.7	146	11	Q924R8	Q924r8 mus musculus
25	425.5	34.5	144	11	Q924P5	Q924p5 mus musculus
26	424	34.4	597	4	Q9BU10	Q9bul10 homo sapien
27	424	34.4	618	4	Q96AA6	Q96aa6 homo sapien
28	420	34.1	597	4	Q9BOB8	Q9bob8 homo sapien
29	419	34.0	145	11	Q924Q7	Q924q7 mus musculus
30	418	33.9	143	11	Q924R0	Q924r0 mus musculus
31	418	33.9	145	11	Q924R3	Q924r3 mus musculus
32	415	33.7	137	11	Q924R6	Q924r6 mus musculus
33	415	33.7	143	11	Q924R7	Q924r7 mus musculus
34	414	33.6	145	11	Q924R1	Q924r1 mus musculus
35	412	33.4	145	11	Q924R4	Q924r4 mus musculus
36	410	33.3	143	11	Q91VA2	Q91va2 mus musculus
37	409.5	33.2	140	11	Q924P8	Q924p8 mus musculus
38	409	33.2	145	11	Q924P7	Q924p7 mus musculus
39	406.5	33.0	146	11	Q924Q3	Q924q3 mus musculus
40	404.5	32.8	613	4	Q96EY0	Q96ey0 homo sapien
41	404	32.8	145	11	Q924Q9	Q924q9 mus musculus
42	404	32.8	145	11	Q924Q6	Q924q6 mus musculus
43	404	32.8	482	11	Q91X92	Q91x92 mus musculus
44	403.5	32.7	140	11	Q924R2	Q924r2 mus musculus
45	401.5	32.6	113	4	Q9UL90	Q9ul90 homo sapien

ALIGNMENTS

RESULT 1

Q921K1 PRELIMINARY; PRT; 278 AA.
AC Q921K1;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE UNKNOWN (PROTEIN FOR MGC:18977).
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC012207; AAH12207.1; -.
SQ SEQUENCE 278 AA; 29778 MW; F894F955DDCD948A CRC64;

Query Match	60.3%	Score 743.5;	DB 11;	Length 278;
Best Local Similarity	60.3%	Pred. NO. 3.1e-59;		
Matches 137;	Conservative 39;	Mismatches 44;	Indels 5;	Gaps 2;
QY	1	EVQLVESGGGLVQPGGSLRLSCATSGYTFETMHWMRQAPGKLEWVAGINPKNGTSH	60	
Db	20	QVQLQPGAEVLVPGASVKLSCKASGYTFISYWNHWYKQRGGQLEWIGINPNSGGTNY	79	
QY	61	NQRFMDRFTISVDKSTSTAYMQMNSLRAEDTAVYICARWRGLNAGFDVRYFDVWGQGLTV	120	
Db	80	NEKFKNKATLAVDKSSSTVTVMQLSSLTSEDSAVYICR----	135	
QY	121	TVSSASTKGSVPPLAPSSKTSGGTAAALCLVKDIPPEPVTVSWNSGALTSGVHPTPAV	180	
Db	136	TVSSAKTTAPSVYPLAPVCGGTGGSSVTLGCLVKGYPEPVTLTWNSGLSSGSHVHTPAL	195	
QY	181	LOSSGLYSLSSVTVVPSSSLGTTQTYICNVNHPKSNTKVDKKVEPK	225	
Db	196	LQ-SGLYTLSSSVTVTSNTWPSQTITCNVAHPASSTKVDKKIEPR	239	

RESULT 7
Q9R1A4
ID Q9R1A4
PRELIMINARY: PRT: 437 AA.

OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC	NCBI_TaxID=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE=PRIMARY B-CELLS FROM TONSILLS;
RA	Strausberg R.;
RL	Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR	EMBL; BC009851; AAH09851.1; -.
SQ	SEQUENCE 614 AA; 67921 MW; 55EF536E77AA9BBB CRC64;
Query Match	40.6%; Score 501; DB 4; Length 614;
Best Local Similarity	45.7%; Pred. No. 6.6e-37;
Matches 101; Conservative 45; Mismatches 65; Indels 10; Gaps	
QY	1 EVOLVESGGGLVOPGSLRSLSCATSGYTFTFYTHMWRQAQGKLEWVAGINPKNGGTSH 60 : : : : : : : : : : : :
Db	20 QMLQVSGAEVKKTGGTSKVSKASGVTFYRYLHWVRQAQGALEMGMWITPFNGNTNY 79 : : : : : : : : : : : :
QY	61 NORPMDRFTISVDKSTSTAYTMWNLSRAEDTAVYYCARWRGLNYGFDFVDMVGQGTLV 120 : : : : : : : : : : : :
Db	80 AQKFQDRTVTIRDSMTATWELSLKSEDTAMYCA--RGYSSTDW-DAFDIWGGQTMV 136 : : : : : : : : : : : :
QY	121 TVSSASTKGFSVPFLAPSSKSTSG-GTAALGCLVKDYFPEPTVSW--NSGALTSGVHTF 177 : : : : : : : : : : : :
Db	137 TVSSGSASPTLPPLVSCENSPSDTSVAVGCQAODFLPDSTITFSWKYKNNSDISSTRGF 196 : : : : : : : : : : : :
QY	178 PVLQSSGLYSLGSVTVTPSSSL--GTQTY-ICNVNHKPSN 215 : : : : : : : : : : : :
Db	197 PSVLR-CGKYAATSQVLPLSKDWQGTDEHVCKVQHPCGN 236 : : : : : : : : : : : :
RESULT 11	
Q91WP5	PRELIMINARY; PRT; 479 AA.
ID	Q91WP5 PRELIMINARY; PRT; 479 AA.
AC	Q91WP5;
DT	01-DEC-2001 (TrEMBLrel. 19, Created)
DT	01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT	01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE	HYPOTHETICAL 51.6 KDA PROTEIN.
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC	NCBI_TaxID=10090;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE=COLON;
RA	Strausberg R.;
RL	Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
DR	EMBL; BC013656; AH13656.1; -.
KW	Hypothetical protein.
SQ	SEQUENCE 479 AA; 51603 MW; ECB2D0877748584F CRC64;

Query Match	40.38;	Score	496.5;	DB	11;	Length	479;
Best Local Similarity	44.4;	Pred. No.	1.2e-36;				
Matches	107;	Conservative	31;	Mismatches	78;	Indels	25;
Gaps	6;						
Qy	1	EVQLVESGGGLVPGGSLRLSCAISGYTFTFTYTHWMRQAPKGLGWAGINPKNGTSH	60				
Db	20	EVQLVESGGGLVPGGSLKLVSCAASGLTFSNYAKMSVRSQSPKRLWVAAINSGNGNTYY	79				
Qy	61	NQRFMDRFTISVDKSTSPAYMOMSLRAEDPAVYCYARWGLNCFDVRYPDVWCGGTLY	120				
Db	80	SDTMKGRFTISRDNAKSTLYIQMSLSLSEDPAFYCYVRG-----GYFDVWAGATAV	130				
Qy	121	TVSSASTKGPSVFPLAAPSCKTSGGTAAALGCLVKDYDPE-PVTVMNSGALTSGVHTTPA	179				
Db	131	TVSSEAPREPTIYPLT-FPQALSDPVIIGLIIHDYFPSPGTMNVTWKGSGKDIITVNFPP	189				
Qy	180	VLOSAGLYSLSSVTVFSSSLGT-QTVICNNVNHKPSNTKVDKKVE-----PKS	226				

```

Db 190 ALASGRYTMSSQLTLPVCEGESVKCSVQH-DSNPVQELNVNCPGICSPPTTPPPPS 248
Qy 227 C 227
    I
Db 249 C 249

RESULT 12
Q91WR1 PRELIMINARY; PRT; 488 AA.
AC Q91WR1:
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE HYPOTHEtical 53.0 KDA PROTEIN.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RN RN
RP RP
RF TISSUE=KIDNEY;
RC Strausberg R.;
RA Submitted (SEP-2001) to the EMBL/GenBank/DBDJ databases.
RL EMBL; BC013539; AAH13539.1; -.
DR Hypothetical protein.
KW SEQUENCE 488 AA; 52964 MW; F12068460B400B9D CRC64;
SQ

```

Query Match	39.7%;	Score 489;	DB 11;	Length 488;
Best Local Similarity	42.3%;	Pred. No. 6e-36;		
Matches 102;	Conservative 42;	Mismatches 81;	Indels 16;	Gaps 5;
Qy	1	EVOLVESGGGLVOPGGSURLSCATSGYTFTEYTMHMRQAPGKLEWVAGINPKNGTSH	60	
Db	20	EVLOQSGPELVKPGASVKLSKASGYTITDYVNVVKQSHGKSLWIGDINPYNGTSY	79	
Qy	61	NOREMDRETTISVDKSTSTAYMOMNSLRADTAVYCARWGLNYCFDVRYPDVWGQGLV	120	
Db	80	NOKFGKATLTVDRSSSTAYMOLNNLTSDSAAVYICARGPVYVFSYDRDGYWGQGLV	139	
Qy	121	TVSSASTKGPSVFPLAPSSKSTSGGTAALGLVLDKDYFPE-PVTVSWNSGALTS	179	
Db	140	TVSAEPAREPTIYPLT-PPQALSSDPVILGLIHDYFFSGTMMNTWGSKGDITTVNPP	198	
Qy	180	VLQSSGLYSLSWTVTPSSSLGT-QTYICNVNHHKPSNTKVDKKVE-----PKS	226	
Db	199	ALASGGRYTMSSQLTLPAVECPGESVKCSVQH-DSNPVQELNVNCPGICSPPTTPPPPS	257	
Qy	227	C	227	
Db	258	C	258	

RESULT	13	
Q99KA4		
ID	Q99KA4	PRELIMINARY;
AC	Q99KA4;	PRT; 487 AA.
DT	01-JUN-2001	(TrEMBLrel. 17, Created)
DT	01-JUN-2001	(TrEMBLrel. 17, Last sequence update)
DT	01-DEC-2001	(TrEMBLrel. 19, Last annotation update)
DE	HYPOTHETICAL 52.6 KDA PROTEIN.	
OS	Mus musculus (Mouse).	
OC	Eukaryota; Metazoa; Chordata; Vertebrata	
OC	Mammalia; Eutheria; Rodentia; Sciurognathi;	
OX	NCBI_TaxID=10090;	
EN	[1]	
RP	SEQUENCE FROM N.A.	
RA	Strausberg R.;	
RL	Submitted (MAR-2001) to the EMBL/GenBank/DDBB	
RR	EMBL; BC004786; AAH04786.1; -.	
DR	HSSP; P01810; 2FBJ.	
DR	InterPro; IPR003599; Ig.	

```
DR InterPro: IPR003597; Ig_cl.
DR InterPro: IPR003600; Ig_like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig_4.
DR SMART: SM00409; Ig; 3.
DR SMART: SM00407; IGcl; 3.
DR SMART: SM00406; IGv; 1.
DR SMART: SM00410; IG_like; 1.
DR PROSITE: PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 487 AA; 52554 MW; 7DC8E96DB333077B CRC64;

Query Match 38.8%; Score 478.5; DB 11; Length 487;
Best Local Similarity 44.4%; Pred. No. 5.3e-35;
Matches 107; Conservative 35; Mismatches 82; Indels 17; Gaps 8;

QY 1 EVLVESGGGLVQPGGSLRLSCATSGYTFETVTHMWRQAPGKLEWVAGINPKNGGTS 60
DQ 1 EVLVESGGGLVQPGGSLRLSCATSGYTFETVTHMWRQAPGKLEWVAGINPKNGGTS 60
DQ 20 EVLVESGGGLVQPGGSLRLSCATSGYTFETVTHMWRQAPGKLEWVAGINPKNGGTS 60
QY 61 NQRFMDRTTISVDKSTAYMNMNSLRADTAAYVCAR-WRGLNYCFDVRVYFDVWGQGL 119
DQ 61 NQRFMDRTTISVDKSTAYMNMNSLRADTAAYVCAR-WRGLNYCFDVRVYFDVWGQGL 119
DQ 80 PDNVKGRFTISRDNKAKNLYLQMSHLKSEDTAMVYCVPEIPERRLEWVAAIT-SGNTYY 138
QY 120 VTVSASTKGPSVFLAPSSKTSGGTAALGCLVKDYFPE-PVTVSWNSGALTSGVHTFP 178
DQ 120 VTVSASTKGPSVFLAPSSKTSGGTAALGCLVKDYFPE-PVTVSWNSGALTSGVHTFP 178
DQ 139 ITVSESARNPTIYPLT-LPRALSSDPVLIIGLIHDPSTGTMNTWGSKGDIITVNPFP 197
QY 179 AVLOSSGLYSLSSVVPSSSLGT-QTYICNVNHRKPSNT--KVDKKVE-----PKS 226
DQ 179 AVLOSSGLYSLSSVVPSSSLGT-QTYICNVNHRKPSNT--KVDKKVE-----PKS 226
DQ 198 PALASGGGYTMSSQLTPAVECPGESVKCSVQH-DSNAVQELDVKCSGPPPPCPPCPPS 256
QY 227 C 227
DQ 227 C 227
DQ 257 C 257
DQ 257 C 257

RESULT 14
Q91207 PRELIMINARY; PRT; 486 AA.
AC Q91207;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE HYPOTHETICAL 52.7 KDA PROTEIN.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC010324; AAH10324.1; -.
DR HSSP; P01789; IMCP.
DR InterPro: IPR003597; Ig_cl.
DR InterPro: IPR003600; Ig_like.
DR InterPro: IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig_4.
DR SMART; SM00409; Ig; 4.
DR SMART; SM00407; IGcl; 2.
DR SMART; SM00406; IGv; 1.
DR SMART; SM00410; IG_like; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 486 AA; 52682 MW; 4FEF835125DA870B CRC64;

Query Match 38.7%; Score 477; DB 11; Length 486;
Best Local Similarity 42.9%; Pred. No. 7.2e-35;
Matches 103; Conservative 36; Mismatches 85; Indels 16; Gaps 7;

QY 1 EVLVESGGGLVQPGGSLRLSCATSGYTFETVTHMWRQAPGKLEWVAGINPKNGGTS 60
DQ 1 EVLVESGGGLVQPGGSLRLSCATSGYTFETVTHMWRQAPGKLEWVAGINPKNGGTS 60
DQ 20 EVLVESGGGLVQPGGSLRLSCATSGYTFETVTHMWRQAPGKLEWVAGINPKNGGTS 60
QY 61 NQRFMDRTTISVDKSTAYMNMNSLRADTAAYVCARWGLNYCFDVRVYFDVWGQGL 120
DQ 61 NQRFMDRTTISVDKSTAYMNMNSLRADTAAYVCARWGLNYCFDVRVYFDVWGQGL 120
DQ 199 PDNVKGRFTISRDNKAKNLYLQMSHLKSEDTAMVYCVPEIPERRLEWVAAIT-SGNTYY 138
QY 121 TVSSASTKGPSVFLAPSSKTSGGTAALGCLVKDYFPE-PVTVSWNSGALTSGVHTFPA 179
```

```
Db 139 TVSESARNPTIYPLT-LPRALSSDPVLIIGLIHDPSTGTMNTWGSKGDIITVNPFP 197
QY 180 VLOSSGLYSLSSVVPSSSLGT-QTYICNVNHRKPSNT--KVDKKVE-----PKSC 227
DQ 180 VLOSSGLYSLSSVVPSSSLGT-QTYICNVNHRKPSNT--KVDKKVE-----PKSC 227
DQ 198 ALASGGGYTMSSQLTPAVECPGESVKCSVQH-DSNAVQELDVKCSGPPPPCPPCPPS 256
RESULT 15
Q9BRV0 PRELIMINARY; PRT; 500 AA.
ID Q9BRV0;
AC Q9BRV0;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE HYPOTHETICAL 54.2 KDA PROTEIN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC005951; AAH05951.1; -.
DR HSSP; P01789; IMCP.
DR InterPro: IPR003599; Ig.
DR InterPro: IPR003597; Ig_cl.
DR InterPro: IPR003600; Ig_like.
DR InterPro: IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig_4.
DR SMART; SM00409; Ig; 4.
DR SMART; SM00407; IGcl; 2.
DR SMART; SM00406; IGv; 1.
DR SMART; SM00410; IG_like; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 500 AA; 54154 MW; 0A9BF43F2A3CC6D9 CRC64;

Query Match 38.7%; Score 477; DB 4; Length 500;
Best Local Similarity 44.7%; Pred. No. 7.5e-35;
Matches 98; Conservative 42; Mismatches 69; Indels 10; Gaps 6;

QY 1 EVLVESGGGLVQPGGSLRLSCATSGYTFETVTHMWRQAPGKLEWVAGINPKNGGTS 60
DQ 20 QVHLVSGAEVMSPGASRVSKTSGYAFHTYIIWVRQAPGQLEWGWISPSDDNTRF 79
QY 61 NQRFMDRTTISVDKSTAYMNMNSLRADTAAYVCARWGLNYG----FDVRYFDVWG 115
DQ 61 NQRFMDRTTISVDKSTAYMNMNSLRADTAAYVCARWGLNYG----FDVRYFDVWG 115
DQ 80 AKKFGQRTVLTDTSTSTVYMELSRLSDDTAAYVCAR-RYCSYSSQNDYIIYMDVWG 138
QY 116 QGTLTVSSASTKGPSVFLAPSSKTSGGTAALGCLVKDYFPE-PVTVSWNSGALTSGV 174
DQ 116 QGTLTVSSASTKGPSVFLAPSSKTSGGTAALGCLVKDYFPE-PVTVSWNSGALTSGV 174
DQ 139 KGTTVTVSSASPTSPKVFPLSLCS-TQPDGNVIACLVQGFQEPLEISVTSSESQGVTA 197
QY 175 HTFPAVLQSSG-LYSLSSVVPSSS-LGTOTYICNVNH 211
DQ 175 HTFPAVLQSSG-LYSLSSVVPSSS-LGTOTYICNVNH 211
DQ 198 RNPPPSODASGDLTYTSSQLTLPATQCLAGKSVTCHVKH 236
```

Search completed: August 14, 2002, 11:07:12
Job time: 382 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 14, 2002, 10:51:59 ; Search time 54.11 Seconds
(without alignments)
476.236 Million cell updates/sec

Title: US-09-811-384-10

Perfect score: 1233

Sequence: 1 EVOLVESGGLVPGGSLRL.....PSNFKVDKVEPKSCDKTHT 232

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_032802.*

1:	/SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1980.DAT.*
2:	/SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1981.DAT.*
3:	/SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1982.DAT.*
4:	/SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1983.DAT.*
5:	/SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1984.DAT.*
6:	/SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1985.DAT.*
7:	/SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1986.DAT.*
8:	/SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1987.DAT.*
9:	/SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1988.DAT.*
10:	/SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1989.DAT.*
11:	/SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1990.DAT.*
12:	/SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1991.DAT.*
13:	/SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1992.DAT.*
14:	/SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1993.DAT.*
15:	/SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1994.DAT.*
16:	/SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1995.DAT.*
17:	/SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1996.DAT.*
18:	/SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1997.DAT.*
19:	/SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1998.DAT.*
20:	/SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1999.DAT.*
21:	/SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA2000.DAT.*
22:	/SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1233	100.0	232	18 AAW34503	Heavy chain of hum
2	1233	100.0	232	20 AAY08753	Human antibody huH
3	1233	100.0	241	20 AAW95614	Humanized anti-CD1
4	1233	100.0	241	22 AAB66776	rhuMAB CD18 heavy
5	1233	100.0	277	20 AAW30631	Recombinant humani
6	1233	100.0	300	20 AAW95623	PS1130 expression
7	1233	100.0	300	22 AAW30635	Recombinant humani
8	1233	100.0	300	22 AAB66785	Protein encoded by
9	1233	100.0	537	21 AAB03664	Anti-CD18 antibody
10	1137	92.2	450	18 AAW34505	Heavy chain of ful
11	1137	92.2	450	20 AAY08755	Human IgG2 huH52 h

12	1116	90.5	552	14	AAW30775	pH52-8.0 humanised
13	1094	88.7	232	17	AAW00374	Anti-CD18 chimeric
14	1091	88.5	454	14	AAW30774	H52H4-160 murine a
15	1030	83.5	253	20	AAW29444	Humanised anti-IL-
16	1030	83.5	253	20	AAW29444	Humanised anti-IL-
17	1030	83.5	253	21	AAW30314	Humanised anti-IL-
18	1030	83.5	253	21	AAW30316	6G4-2-5V11 heavy c
19	1030	83.5	253	21	AAW77757	Humanised anti-IL-
20	1030	83.5	253	21	AAW77759	Humanised anti-IL-
21	1030	83.5	256	19	AAW69304	Humanised anti-IL-
22	1030	83.5	256	20	AAW29457	6G4V1N35A Fab' he
23	1030	83.5	256	21	AAW30321	Humanised anti-IL-
24	1030	83.5	256	21	AAW77765	Humanised anti-IL-
25	1030	83.5	298	19	AAW69303	Humanised anti-IL-
26	1030	83.5	298	20	AAW29456	Humanised anti-IL-
27	1030	83.5	298	21	AAW30319	Humanised anti-IL-
28	1030	83.5	298	21	AAW77762	Anti-IL-8 6G4-2-5V
29	1030	83.5	452	20	AAW29458	Humanised anti-IL-
30	1030	83.5	452	21	AAW30322	Recombinant immuno
31	1030	83.5	452	21	AAW77766	Humanised anti-IL-
32	1021	82.8	452	19	AAW69316	Anti-IL-8 humanise
33	1007.5	81.7	412	19	AAW70672	Protein encoded by
34	989	80.2	461	13	AAW24048	Heavy chain of 4D5
35	989	80.2	527	22	AAW82925	Anti-HER2 HuMab4D5
36	989	80.2	698	20	AAW83493	4D5 Fab molecule e
37	980.5	79.5	449	21	AAW68810	A rat heavy chain
38	966.5	78.4	229	20	AAW56655	Mus musculus anti-
39	966.5	78.4	229	22	AAW76954	Variable heavy cha
40	966.5	78.4	233	20	AAW95670	Mus musculus anti-
41	966.5	78.4	233	22	AAW76959	Variable heavy cha
42	966.5	78.4	451	20	AAW95659	Mus musculus anti-
43	966.5	78.4	451	20	AAW95661	Mus musculus anti-
44	966.5	78.4	451	21	AAW85201	Light chain amino
45	966.5	78.4	451	22	AAW47088	Anti-IgE antibody,

ALIGNMENTS

RESULT	1
AAW34503	
ID AAW34503 standard; protein; 232 AA.	
XX	
AC AAW34503;	
XX	
DT 19-MAR-1998 (first entry)	
XX	
DE Heavy chain of humanised H52 antibody.	
XX	
KW Humanised antibody; HuH52; heavy chain; focal ischaemic stroke; embolism;	
KW brain damage; anti-CD18 antibody; cerebral blood flow; thromboembolism;	
KW transient ischaemic attack; thrombolytic therapy; thrombosis; therapy;	
KW systemic hypoperfusion; cardiac arrest.	
XX	
OS Synthetic.	
OS Homo sapiens.	
OS Mus sp.	
XX	
PN WO926912-A2.	
XX	
PD 31-JUL-1997.	
XX	
PF 11-JAN-1997; 97WO-US00492.	
XX	
PR 23-JAN-1996; 96US-0589982.	
XX	
PA (GETH) GENENTECH INC.	
PA (UYVE-) UNIV VERMONT & STATE AGRIC COLLEGE.	
PI Bednar MM, Gross CE, Thomas GR;	
XX WPI; 1997-393373/36.	
DR	


```

XX PF 12-JUN-1998; 98WO-US12209.
XX PI 13-JUN-1997; 97US-0874897.
XX PA (GETH ) GENENTECH INC.
XX PI Lam XM, Oeswein JQ, Ongpipattanakul B, Shahrokh Z;
XX PI Wang SX, Weissburg RP, Wong RL;
XX DR WPI; 1999-080860/07.
XX XX Stable aqueous antibody formulations - comprising an antibody
PT not subjected to lyophilization, a buffer maintaining the pH at 4.5
PT - 6, a surfactant and a polyol
XX PS Disclosure; Fig 1A; 87pp; English.
XX CC The sequence is that of the heavy chain of a humanized murine
CC anti-CD18 antibody rhuMAB CD18. It can be used for the treatment
CC of disorders which include haemorrhagic shock, thermal injury (such
CC as that resulting from burns), stroke (including ischaemic and
CC haemorrhagic stroke) and myocardial infarction. The antibody
CC formulation can be stabilised at a temperature of 2-8 deg. C
CC for at least one year or at a temperature of 30 deg. C for at
CC least one month and is stable following freezing and thawing.
XX SQ Sequence 241 AA;

Query Match 100.0%; Score 1233; DB 20; Length 241;
Best Local Similarity 100.0%; Pred. No. 4.7e-88;
Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVQPGGSLRLSCATGYFTFTYTHMWRQAPGKLEWVAGINPKNGGTS 60
DB 1.evqlvesggglvqpggsirlscatsgyftftymhwmrqapkgkglewvaginpknggtsh 60
QY 61 NQRFMDRTISVDKSTAYMQMNSLRADTAIVYCARWRGLNYGDFVYFDVWGQGLTV 120
DB 61 nqrfmdrtisvdkststaymqmnsiraedtavyycarwrglnygfdfvryfdvwgqgltv 120
QY 121 TVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAV 180
DB 121 tvssastkgpsvfplapskstsaggtaalgclvkdypfpvsvwnsgaltsgvhtfpav 180
QY 181 LQSSGLYSLSVVTVPSSSLGTQTYICNVNHPKPSNTKVDKKVEPKSCDKTHT 232
DB 181 lqssglyslsvvtvpssslgtqtyicnvnhkpsntkvdkkvepkscdktht 232

RESULT 4
AAB66776
ID AAB66776 standard; protein; 241 AA.
XX AC AAB66776;
XX DT 10-APR-2001 (first entry)
XX DE rhuMAB CD18 heavy chain.
XX KW Antibody; lyophilization; hemorrhagic shock; thermal injury;
XX KW myocardial infarction; inflammation.
XX OS Homo sapiens.
XX PN US6171586-B1.
XX PD 09-JAN-2001.
XX PF 12-JUN-1998; 98US-0097171.
XX PR 13-JUN-1997; 97US-0053087.

XX PF 12-JUN-1998; 98WO-US12209.
XX PI 13-JUN-1997; 97US-0874897.
XX PA (GETH ) GENENTECH INC.
XX PI Lam XM, Oeswein JQ, Ongpipattanakul B, Shahrokh Z;
XX PI Wang SX, Weissburg RP, Wong RL;
XX DR WPI; 2001-136863/14.
XX XX Stable aqueous pharmaceutical formulation for treating hemorrhagic
PT shock, thermal injury, stroke, and myocardial infarction, comprises an
PT antibody not subjected to prior lyophilization -
XX PS Example 1; Fig 1; 56pp; English.
XX CC The present invention relates to a stable aqueous pharmaceutical
CC formulation, comprising an antibody not subjected to prior
CC lyophilization, an acetate buffer of pH 4.8-5.5, a surfactant and
CC a polyol. The invention is useful for treating hemorrhagic shock,
CC thermal injury, e.g. resulting from burns, stroke including
CC ischemic and hemorrhagic stroke, myocardial infarction,
CC inflammatory disorders such as adult respiratory distress
CC syndrome (ARDS), hypovolemic shock, ulcerative colitis, rheumatoid
CC arthritis and B-cell lymphomas.
XX SQ Sequence 241 AA;

Query Match 100.0%; Score 1233; DB 22; Length 241;
Best Local Similarity 100.0%; Pred. No. 4.7e-88;
Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVQPGGSLRLSCATGYFTFTYTHMWRQAPGKLEWVAGINPKNGGTS 60
DB 1.evqlvesggglvqpggsirlscatsgyftftymhwmrqapkgkglewvaginpknggtsh 60
QY 61 NQRFMDRTISVDKSTAYMQMNSLRADTAIVYCARWRGLNYGDFVYFDVWGQGLTV 120
DB 61 nqrfmdrtisvdkststaymqmnsiraedtavyycarwrglnygfdfvryfdvwgqgltv 120
QY 121 TVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAV 180
DB 121 tvssastkgpsvfplapskstsaggtaalgclvkdypfpvsvwnsgaltsgvhtfpav 180
QY 181 LQSSGLYSLSVVTVPSSSLGTQTYICNVNHPKPSNTKVDKKVEPKSCDKTHT 232
DB 181 lqssglyslsvvtvpssslgtqtyicnvnhkpsntkvdkkvepkscdktht 232

RESULT 5
AAW30631
ID AAW30631 standard; protein; 277 AA.
XX AC AAW30631;
XX DT 06-APR-1999 (first entry)
XX DE Recombinant humanised anti-CD18 antibody rhuMAB CD18 heavy chain.
XX KW Recombinant humanised anti-CD18 antibody; rhuMAB CD18; leucine zipper;
XX KW murine monoclonal antibody; muMAB H52; protein recovery; filtration;
XX KW chromatography.
XX OS Mus sp.
XX OS Homo sapiens.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT Region 242..277
XX FT /label= leucine_zipper
XX PN WO9856808-A1.
XX PR 17-DEC-1998.

```

XX PF 12-JUN-1998; 98WO-US12334.
 XX PR 13-JUN-1997; 97US-0050951.
 XX PA (GETH) GENENTECH INC.
 XX PI Blank GS, Narindray DS, Zapata GA;
 XX DR WPI; 1999-060267/05.
 XX PR New method for recovering polypeptides from cell cultures - by
 PT treating with reagent and filtering to remove reagent
 XX PS Example; Fig 1A; 43pp; English.
 XX CC A method has been developed for recovering a polypeptide comprising: (a)
 CC exposing a composition comprising a polypeptide to a reagent which binds
 CC to or modifies the polypeptide, where the reagent is immobilized on a
 CC solid phase; and (b) passing the composition through a filter bearing an
 CC opposite charge to the reagent so as to remove leached reagent from the
 CC composition. The present invention also describes a method for modifying
 CC a precursor antibody comprising a leucine zipper by exposing the
 CC precursor antibody to a protease immobilized on a solid support so that
 CC the protease removes the zipper. The methods can be used to purify
 CC proteins from cell cultures. They are especially useful for isolating
 CC antibodies. The methods overcome the problem of reagent leakage into the
 CC protein as is the case in prior art immobilized modification systems. By
 CC using a opposite charge filter the reagent can be excluded from the
 CC sample, preventing contamination. The present sequence represents the
 CC recombinant humanised anti-CD18 antibody (rhuMab CD18) heavy chain,
 CC which is used in an example from the present invention.
 XX SQ Sequence 277 AA;

Query Match 100.0%; Score 1233; DB 20; Length 277;
 Best Local Similarity 100.0%; Pred. No. 5.5e-88;
 Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EVLVESGGGLVPGGSLRLSCATSGYTFEYTHMWRQAPGKLEWVAGINPKNGTSH 60
 Db 1 evqlvesggglvpggslrlscatsgytfttymhwrqapkglewaginpknngtsh 60
 QY 61 NQRFMDRTISVDKSTSTAYMQMNSLRAEDTAVYYCARWRGLNYGFDVRYFDVWGQGLTV 120
 Db 61 nqrfmdrtisvdkststaymqmnsrlraedtavyycarwrglnygfdvryfdvwwgqgltv 120
 QY 121 TVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAV 180
 Db 121 tvssastkgpsvfpplapsskstsggtaalgclvkdypfpptvswnsgaltsgvhtfpav 180
 QY 181 LQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNTKVDKVKPEKSCDKTHT 232
 Db 181 lqssgylslssvvtvpssslgtqtyicnvnhkpsntkvdkvpekscdktht 232

RESULT 6
 AAW95623
 ID AAW95623 standard; Protein; 300 AA.
 XX AC AAW95623;
 XX DT 08-JUN-1999 (first entry)
 XX DE pS1130 expression cassette encoded rhuMab CD18 heavy chain.
 XX KW Monoclonal antibody; heavy chain; humanized; myocardial infarction;
 KW burns; thermal injury; ischemic; shock; ischaemic; haemorrhagic;
 KW hemorrhagic; stroke; heavy chain.
 XX Mus musculus.
 OS Synthetic.

XX FH Key Location/Qualifiers
 XX sig_peptide 1..23
 XX PN WO9856418-A1.
 XX PD 17-DEC-1998.
 XX PF 12-JUN-1998; 98WO-US12209.
 XX PR 13-JUN-1997; 97US-0874897.
 XX PA (GETH) GENENTECH INC.
 XX PI Lam XM, Oeswein JQ, Ongpipattanakul B, Shahrokhi Z;
 PI Wang SX, Weissburg RP, Wong RL;
 XX WPI; 1999-080860/07.
 XX DR New stable aqueous antibody formulations - comprising an antibody
 PT not subjected to lyophilisation, a buffer maintaining the pH at 4.5
 PT - 6, a surfactant and a polyol
 XX PS Disclosure; Fig 21A; 87pp; English.
 XX CC The sequence is that of the pS1130 encoded heavy chain of a humanized
 CC murine anti-CD18 antibody rhuMab CD18. It can be used for the treatment
 CC of disorders which include haemorrhagic shock, thermal injury (such
 CC as that resulting from burns), stroke (including ischaemic and
 CC haemorrhagic stroke) and myocardial infarction. The antibody
 CC formulation can be stabilised at a temperature of 2-8 deg. C
 CC for at least one year or at a temperature of 30 deg. C for at
 CC least one month and is stable following freezing and thawing.
 XX SQ Sequence 300 AA;

Query Match 100.0%; Score 1233; DB 20; Length 300;
 Best Local Similarity 100.0%; Pred. No. 6.1e-88;
 Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EVLVESGGGLVPGGSLRLSCATSGYTFEYTHMWRQAPGKLEWVAGINPKNGTSH 60
 Db 24 evqlvesggglvpggslrlscatsgytfttymhwrqapkglewaginpknngtsh 83
 QY 61 NQRFMDRTISVDKSTSTAYMQMNSLRAEDTAVYYCARWRGLNYGFDVRYFDVWGQGLTV 120
 Db 84 nqrfmdrtisvdkststaymqmnsrlraedtavyycarwrglnygfdvryfdvwwgqgltv 143
 QY 121 TVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAV 180
 Db 144 tvssastkgpsvfpplapsskstsggtaalgclvkdypfpptvswnsgaltsgvhtfpav 203
 QY 181 LQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNTKVDKVKPEKSCDKTHT 232
 Db 204 lqssgylslssvvtvpssslgtqtyicnvnhkpsntkvdkvpekscdktht 255

RESULT 7
 AAW30635
 ID AAW30635 standard; protein; 300 AA.
 XX AC AAW30635;
 XX DT 06-APR-1999 (first entry)
 XX DE Recombinant humanised anti-CD18 antibody rhuMab CD18 heavy chain.
 XX KW Recombinant humanised anti-CD18 antibody; rhuMab CD18; leucine zipper;
 KW murine monoclonal antibody; muMab H52; protein recovery; filtration;
 KW chromatography.
 XX Mus sp.

OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Peptide 1..23
FT /label= signal
XX
XX WO9856808-A1.
XX
XX 17-DEC-1998.
XX
XX 12-JUN-1998; 98WO-US12334.
XX
XX 13-JUN-1997; 97US-0050951.
XX
XX (GETH) GENENTECH INC.
XX
XX Blank GS, Narindray DS, Zapata GA;
XX WPI; 1999-060267/05.
XX N-PSDB; AAX03840.
XX
XX New method for recovering polypeptides from cell cultures - by
XX treating with reagent and filtering to remove reagent
XX
XX Example; Fig 4; 43pp; English.
XX
XX A method has been developed for recovering a polypeptide comprising: (a)
XX exposing a composition comprising a polypeptide to a reagent which binds
XX to or modifies the polypeptide, where the reagent is immobilized on a
XX solid phase; and (b) passing the composition through a filter bearing an
XX opposite charge to the reagent so as to remove leached reagent from the
XX composition. The present invention also describes a method for modifying
XX a precursor antibody comprising a leucine zipper by exposing the
XX precursor antibody to a protease immobilized on a solid support so that
XX the protease removes the zipper. The methods can be used to purify
XX proteins from cell cultures. They are especially useful for isolating
XX antibodies. The methods overcome the problem of reagent leakage into the
XX protein as is the case in prior art immobilized modification systems. By
XX using a opposite charge filter the reagent can be excluded from the
XX sample, preventing contamination. The present sequence represents the
XX recombinant humanised anti-CD18 antibody (rhMAB CD18) heavy chain,
XX which is used in an example from the present invention.
XX
SQ Sequence 300 AA;

Query Match 100.0%; Score 1233; DB 20; Length 300;
Best Local Similarity 100.0%; Pred. No. 6.le-88;
Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVQPGGSLRLSCATSGYTFETYMHWMRQAPGKLEWVAGINPKNGGTS 60
DB 24 EVQLVESGGGLVQPGGSLRLSCATSGYTFETYMHWMRQAPGKLEWVAGINPKNGGTS 83
QY 61 NORFMDRTISVDKSTSTAYMQMNSLRAEDTAVYICARWGLNYGFDVRYFDVWGQGLTV 120
DB 84 NQRFMDRTISVDKSTSTAYMQMNSLRAEDTAVYICARWGLNYGFDVRYFDVWGQGLTV 143
QY 121 TVSSASTKGPSVFPPLAPSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHFPFAV 180
DB 144 TVSSASTKGPSVFPPLAPSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHFPFAV 203
QY 181 LQSSGLYSLSSVWTPVSSSLGTQTYICNVNHPKSNNTKVDKKVEPKSCDKTHT 232
DB 204 LQSSGLYSLSSVWTPVSSSLGTQTYICNVNHPKSNNTKVDKKVEPKSCDKTHT 255

RESULT 8
AAB66785
ID AAB66785 standard; protein; 300 AA.
XX
AC AAB66785;

Query Match 100.0%; Score 1233; DB 22; Length 300;
Best Local Similarity 100.0%; Pred. No. 6.le-88;
Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVQPGGSLRLSCATSGYTFETYMHWMRQAPGKLEWVAGINPKNGGTS 60
DB 24 EVQLVESGGGLVQPGGSLRLSCATSGYTFETYMHWMRQAPGKLEWVAGINPKNGGTS 83
QY 61 NORFMDRTISVDKSTSTAYMQMNSLRAEDTAVYICARWGLNYGFDVRYFDVWGQGLTV 120
DB 84 NQRFMDRTISVDKSTSTAYMQMNSLRAEDTAVYICARWGLNYGFDVRYFDVWGQGLTV 143
QY 121 TVSSASTKGPSVFPPLAPSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHFPFAV 180
DB 144 TVSSASTKGPSVFPPLAPSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHFPFAV 203
QY 181 LQSSGLYSLSSVWTPVSSSLGTQTYICNVNHPKSNNTKVDKKVEPKSCDKTHT 232
DB 204 LQSSGLYSLSSVWTPVSSSLGTQTYICNVNHPKSNNTKVDKKVEPKSCDKTHT 255

RESULT 9
AAB03664
ID AAB03664 standard; Protein; 537 AA.
XX
AC AAB03664;

QY 04-OCT-2000 (first entry)
XX

XX 10-APR-2001 (first entry)
XX
XX Protein encoded by ps 1130 expression cassette.
XX
XX Antibody; lyophilization; hemorrhagic shock; thermal injury;
XX myocardial infarction; inflammation.
XX
XX Homo sapiens.
XX
XX US6171586-B1.
XX
XX 09-JAN-2001.
XX
XX 12-JUN-1998; 98US-0097171.
XX
XX 13-JUN-1997; 97US-0053087.
XX
XX (GETH) GENENTECH INC.
XX
XX Lam XM, Oeswein JQ, Ongpipattanakul B, Shahrokh Z, Wang SX;
XX Weissburg RP, Wong RL;
XX WPI; 2001-136863/14.
XX
XX Stable aqueous pharmaceutical formulation for treating hemorrhagic
XX shock, thermal injury, stroke, and myocardial infarction, comprises an
XX antibody not subjected to prior lyophilization -
XX
XX Disclosure; Fig 21; 56pp; English.
XX
XX The present invention relates to a stable aqueous pharmaceutical
XX formulation, comprising an antibody not subjected to prior
XX lyophilization, an acetate buffer of pH 4.8-5.5, a surfactant and
XX a polyol. The invention is useful for treating hemorrhagic shock,
XX thermal injury, e.g. resulting from burns, stroke including
XX ischemic and hemorrhagic stroke, myocardial infarction,
XX inflammatory disorders such as adult respiratory distress
XX syndrome (ARDS), hypovolemic shock, ulcerative colitis, rheumatoid
XX arthritis and B-cell lymphomas.
XX
SQ Sequence 300 AA;

Query Match 100.0%; Score 1233; DB 22; Length 300;
Best Local Similarity 100.0%; Pred. No. 6.le-88;
Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVQPGGSLRLSCATSGYTFETYMHWMRQAPGKLEWVAGINPKNGGTS 60
DB 24 EVQLVESGGGLVQPGGSLRLSCATSGYTFETYMHWMRQAPGKLEWVAGINPKNGGTS 83
QY 61 NORFMDRTISVDKSTSTAYMQMNSLRAEDTAVYICARWGLNYGFDVRYFDVWGQGLTV 120
DB 84 NQRFMDRTISVDKSTSTAYMQMNSLRAEDTAVYICARWGLNYGFDVRYFDVWGQGLTV 143
QY 121 TVSSASTKGPSVFPPLAPSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHFPFAV 180
DB 144 TVSSASTKGPSVFPPLAPSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHFPFAV 203
QY 181 LQSSGLYSLSSVWTPVSSSLGTQTYICNVNHPKSNNTKVDKKVEPKSCDKTHT 232
DB 204 LQSSGLYSLSSVWTPVSSSLGTQTYICNVNHPKSNNTKVDKKVEPKSCDKTHT 255

RESULT 9
AAB03664
ID AAB03664 standard; Protein; 537 AA.
XX
AC AAB03664;

QY 04-OCT-2000 (first entry)
XX

DE Anti-CD18 antibody (rhUMAB CD18) light and heavy chain protein sequence.
XX Expression cassette; pS1130; rhUMAB CD18; monoclonal antibody;
KW biochemical lysis; polypeptide recovery; anti-CD18 antibody.
XX Synthetic.
XX Key Location/Qualifiers
FH 1..248
FT Region /note= "Anti-CD18 light chain"
FT 249..537
FT Region /note= "Anti-CD18 heavy chain"
XX
XX WO200024873-A1.
XX
XX 04-MAY-2000.
XX
XX 21-OCT-1999; 99WO-US24696.
XX
XX 28-OCT-1998; 98US-0106052.
XX
XX (GETH) GENENTECH INC.
XX Leung WS, Swartz JR;
PI
XX WPI; 2000-350719/30.
DR N-PSDB; AAA53339, AAA53389.
XX
XX Process for large scale production and recovery of polypeptides from
PT bacterial cells using a method of biochemical lysis -
XX
XX Example 1; Fig 4; 64pp; English.
XX
XX This sequence represents the anti-CD18 antibody (rhUMAB CD18) light and
CC heavy chain amino acid sequences. RhUMAB CD18 is a recombinant F(ab')₂
CC antibody, which binds to the MAC-1 (CD11b/CD18) receptor, blocking
CC binding of neutrophils to the endothelium. The expression cassette is
CC used in an example of the process of the invention, for recovering a
CC heterologous polypeptide from bacterial cells using biochemical lysis.
CC The process is used for the large scale production and recovery of
CC polypeptides e.g. human insulin-like growth factor (IGF), DNase, vascular
CC endothelial growth factor (VEGF), anti-CD18 antibody or anti-CD18
CC antibody fragment from bacterial cells.
XX
XX Sequence 537 AA;
SQ

Query Match 100.0%; Score 1233; DB 21; Length 537;
Best Local Similarity 100.0%; Pred. No. 1.2e-87;
Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVQLVSGGGLVQPGGSLRLSCATSGYFTFTYTHMWRQAPGKGLEWVAGINPKNGGTS 60
DB 261 evqlvesggglvqp9gsrlscatsgyftfeytmhmwrqapkgglewaginpknggts 320

QY 61 NQRFMDRFTTISVDKSTSTAYMQMNSLRAEDTAVYYCARWRGLNYGFDVRYFDVWGQGT 120
DB 321 nqrfmdrftisvdkststaymqmnsraedtavyycarwrglnygfdrvfdvwwggtlv 380

QY 121 TVSSASTKGPSVFPLAPSSKSTSGGTAALGLCLVKDYFPEPVTVSWNSGALTSGVHTFPA 180
DB 381 tvssastkgpsvfplapsskstsggtaalgclvkdypfpvptvswnsgaltsgvhtfpav 440

QY 181 LOSGLYSLSSVWTVPPSSSLGTQTICNVNHKPSNTKVDKKVEPKSCDKTHT 232
DB 441 lqsglyslssvwtvppssslgtqticyinvnhkpsntkvdkkvepkscdktht 492

RESULT 10
AAW34505
ID AAW34505 standard; protein; 450 AA.
XX
AC AAW34505;

XX 19-MAR-1998 (first entry)
DT Heavy chain of full length IgG2 humanised H52 antibody.
XX
XX Humanised antibody; HuH52; heavy chain; focal ischaemic stroke; embolism;
DE brain damage; anti-CD18 antibody; cerebral blood flow; thromboembolism;
KW transient ischaemic attack; thrombolytic therapy; thrombosis; therapy;
KW systemic hypoperfusion; cardiac arrest.
XX Synthetic.
OS Homo sapiens.
OS Mus sp.
XX WO9726912-A2.
XX 31-JUL-1997.
PD
XX 11-JAN-1997; 97WO-US00492.
PF
XX 23-JAN-1996; 96US-0589982.
PR
XX (GETH) GENENTECH INC.
PA (UYVE-) UNIV VERMONT & STATE AGRIC COLLEGE.
PA
XX Bednar MM, Gross CE, Thomas GR;
PI WPI; 1997-393373/36.
DR
XX Administering an anti-CD18 antibody to treat focal ischaemic stroke
PT - by increasing cerebral blood flow and reducing size of brain
PT infarct
PT
XX Disclosure; Page 9; 41pp; English.
XX
XX This sequence represents the heavy chain of the humanised H52 antibody.
CC The H52 antibody can be used in the method of the invention. The method
CC is for treating focal ischaemic stroke, i.e. damage to the brain due to
CC interrupted blood supply, in a mammal, caused by obstruction of a main
CC cerebral artery, comprises administering anti-CD18 antibody to increase
CC cerebral blood flow and/or reduce the size of the area of brain that
CC dies, without removing the arterial obstruction. CD18, is upregulated in
CC patients after ischaemic stroke or transient ischaemic attack (stroke
CC symptoms last less than 24 hours with complete recovery). Treatment with
CC anti-CD18 antibodies can increase cerebral blood flow and/or reduce brain
CC infarct size, improving clinical outcomes in focal ischaemic strokes in
CC mammals, particularly in humans. The method provides an alternative to
CC thrombolytic therapy for treating ischaemic strokes caused by
CC thromboembolism (thrombosis or embolism), particularly where thrombolytic
CC therapy has been unsuccessful, is contra-indicated e.g. because such
CC drugs exacerbate bleeding, or is unsuitable because of the time delay
CC between stroke onset and diagnosis. Thrombolytic agents (e.g. tissue
CC plasminogen activator) may also be administered before, after or
CC simultaneously with the anti-CD18 antibody. Alternatively, the method can
CC be used to treat the third main type of ischaemic stroke, systemic
CC hypoperfusion, e.g. resulting from cardiac arrest or drowning.
XX
XX Sequence 450 AA;
SQ

Query Match 92.2%; Score 1137; DB 18; Length 450;
Best Local Similarity 94.7%; Pred. No. 2.6e-80;
Matches 215; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 1 EVQLVSGGGLVQPGGSLRLSCATSGYFTFTYTHMWRQAPGKGLEWVAGINPKNGGTS 60
DB 1 evqlvesggglvqp9gsrlscatsgyftfeytmhmwrqapkgglewaginpknggts 60

QY 61 NQRFMDRFTTISVDKSTSTAYMQMNSLRAEDTAVYYCARWRGLNYGFDVRYFDVWGQGT 120
DB 61 nqrfmdrftisvdkststaymqmnsraedtavyycarwrglnygfdrvfdvwwggtlv 120

QY 121 TVSSASTKGPSVFPLAPSSKSTSGGTAALGLCLVKDYFPEPVTVSWNSGALTSGVHTFPA 180

```

Db 121 tvssastkpsvflapscrstsestaalgcldvkdypfpvvtvswnsгалтsgvhtfpav 180
      |||
QY 181 LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHNKPSNTKVDKKVEPKSC 227
      |||
Db 181 lqssglyslssvvtvssnfgtqtcnvdhkpnsntkvdktverkcc 227
      |||

RESULT 11
AAY08755
ID AAY08755 standard; protein; 450 AA.
XX
AC AAY08755;
XX
DT 10-AUG-1999 (first entry)
XX
DE Human IgG2 huH52 heavy chain protein fragment.
XX
KW IgG; immunoglobulin G; CH1 domain; human; anti-CD18; IgG1; IgG2; IgG3;
KW IgG4; Kappa-CL domain; lambda-CL domain; focal ischaemic stroke;
KW cerebroprotective; cerebral artery obstruction; blood flow; infarct;
KW CD18 extracellular domain; endothelium; CD18/CD18 complex dissociation;
KW antibody; huH52; heavy chain.
XX
OS Homo sapiens.
XX
PN US5914112-A.
XX
PD 22-JUN-1999.
XX
PF 22-JAN-1997; 97US-0788800.
XX
PR 23-JAN-1996; 96US-0093038.
XX
PR 22-JAN-1997; 97US-0788800.
XX
PA (GETH ) GENENTECH INC.
PA (UYVE-) UNIV VERMONT & STATE AGRIC COLLEGE.
XX
PI Bednar MM, Gross CE, Thomas GR;
XX
DR WPI; 1999-370483/31.
XX
XX Anti-CD18 antibodies in stroke
XX
XX Disclosure; Column 31-34; 25pp; English.
XX
XX This invention describes a method for improving the clinical outcome in
XX focal ischaemic stroke by administering novel anti-CD18 antibody which
XX has cerebroprotective properties. The invention particularly describes a
XX method of treating focal ischaemic stroke caused by the obstruction of a
XX main cerebral artery which comprises administering an anti-CD18 antibody
XX to increase the blood flow or reduce the infarct size, where: (1) the
XX antibody binds to an extracellular domain of CD18 and inhibits or reduces
XX the ability of the cell expressing CD18 to bind to endothelium, (2) the
XX antibody binds CD18 with an affinity of less than 4 nm, or (3) the
XX antibody dissociates CD18/CD18 complex. This sequence represents the
XX human IgG 2 huH52 heavy chain region.
XX
SQ Sequence 450 AA;

Query Match 92.2%; Score 1137; DB 20; Length 450;
Best Local Similarity 94.7%; Pred. No. 2.6e-80;
Matches 215; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVQPGGSLRLSCATSGYTFEYTMHMRQAPGKGLEWVAGINPKNGGTS 60
Db 1 evqlvesggglvqp99gslrlscatsgytfeytmhmwrqapkgglewvaginpknggtsh 60
QY 61 NQRFMDRTISVDKSTAYQMNSLRAEDTAVYICARWRGLNYGFDVRYFDVWGQGLTV 120
Db 61 nqrfdmrdftisvdkststaymqmnsiraedtavyycarwrglnygfdrvfdvwgqgtlv 120
QY 61 nqrfdmrdftisvdkststaymqmnsiraedtavyycarwrglnygfdrvfdvwgqgtlv 120

```

```

QY 121 TVSSASTKGPSVFLAPSSKSTSGGTAALGCLVKDYKPEPEPTVTSWNSGALTSGVHTFP 180
Db 121 tvssastkgpsvflapscrstsestaalgcldvkdypfpvvtvswnsгалтsgvhtfpav 180
QY 181 LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHNKPSNTKVDKKVEPKSC 227
Db 181 lqssglyslssvvtvssnfgtqtcnvdhkpnsntkvdktverkcc 227

RESULT 12
AAR30775
ID AAR30775 standard; protein; 552 AA.
XX
AC AAR30775;
XX
DT 12-MAY-1993 (first entry)
XX
DE pH52-8.0 humanised murine anti-CD18 antibody heavy chain.
KW Humanisation; rapid; monoclonal antibody.
XX
OS Mus musculus.
XX
PN WO9222653-A.
XX
PD 23-DEC-1992.
XX
PF 15-JUN-1992; 92WO-US05126.
XX
PR 14-JUN-1991; 91US-0715272.
XX
PA (GETH ) GENENTECH INC.
XX
PI Carter PJ, Presta LG;
XX
XX WPI; 1993-018139/02.
XX
XX Humanisation of antibodies - by molecular modelling of the variable
XX domains and alteration by gene conversion mutagenesis
XX
XX Disclosure; Fig 6A; 126pp; English.
XX
XX The sequence is that of the humanised heavy chain sequence of
XX murine anti-CD18 antibody pH52-8.0.
XX
SQ Sequence 552 AA;

Query Match 90.5%; Score 1116; DB 14; Length 552;
Best Local Similarity 93.4%; Pred. No. 1.4e-78;
Matches 212; Conservative 3; Mismatches 12; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVQPGGSLRLSCATSGYTFEYTMHMRQAPGKGLEWVAGINPKNGGTS 60
Db 53 evqlvesggglvqp99gslrlscatsgytfeytmhmwrqapkgglewvaginpknggtsh 112
QY 61 NQRFMDRTISVDKSTAYQMNSLRAEDTAVYICARWRGLNYGFDVRYFDVWGQGLTV 120
Db 113 nqrfdmrdftisvdkststaymqmnsiraedtavyycarwrglnygfdrvfdvwgqgtlv 172
QY 121 TVSSASTKGPSVFLAPSSKSTSGGTAALGCLVKDYKPEPEPTVTSWNSGALTSGVHTFP 180
Db 173 tvssastkgpsvflapscrstsestaalgcldvkdypfpvvtvswnsгалтsgvhtfpav 232
QY 181 LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHNKPSNTKVDKKVEPKSC 227
Db 233 lqssglyslssvvtvssnfgtqtcnvdhkpnsntkvdktverkcc 279

RESULT 13
AAW00374
ID AAW00374 standard; Protein; 232 AA.
XX

```

```

AC AAW00374;
XX
DT 24-JAN-1997 (first entry)
XX
DE Anti-CD18 chimeric antibody MHM23 heavy chain.
XX
KW Antibody purification; low pH hydrophobic interaction chromatography;
KW monoclonal antibody; chimeric antibody; humanised antibody; MHM23;
KW heavy chain.
XX
OS Synthetic.
XX
PN WO9633208-A1.
XX
PD 24-OCT-1996.
XX
XX 05-APR-1996; 96WO-US04683.
XX
XX 20-APR-1995; 95US-0425763.
XX
XX (GETH ) GENENTECH INC.
XX
XX Rinderknecht EH, Zapata GA;
XX
XX WPI; 1996-485726/48.
XX
XX Antibody purification by low pH hydrophobic interaction
XX chromatography - allows isolation of correctly folded and
XX disulphide bonded antibodies
XX
PS Example 1; Page 26-27; 41pp; English.
XX
XX The heavy chain (AAW00374) and light chain (AAW00373) of a chimeric
XX version of anti-CD18 monoclonal antibody MHM23 were used to
XX demonstrate a novel technique for antibody purification. Low pH
XX hydrophobic interaction chromatography provides for the purification
XX of correctly-folded and disulphide-bonded antibody fragments from
XX unwanted contaminants. The antibody compsns. obtd. are at least 95%
XX pure.
XX
XX Sequence 232 AA;
XX

Query Match 88.7%; Score 1094; DB 17; Length 232;
Best Local Similarity 86.2%; Pred. No. 2.7e-77;
Matches 200; Conservative 17; Mismatches 15; Indels 0; Gaps 0;

QY 1 EVLVESGGGLVOPGSLRLSCATSGYTFETMHWMRQAPGKGLWVAGINPKNGTSH 60
Db 1 evlqsggpelvkpgavskiscktsgytfttymhmksqshgkslewlgfnpknggssh 60

QY 61 NORFMDRFTISVDKSTSTAYMQMNSLRADTAVYYCARWRGLNYGDFVRYFDVWGOGTLV 120
Db 61 nqrfmdkatlavdkststaymelrsltsedsgiyycarwrglnygfdfvryfdvwgagttv 120

QY 121 TVSSASTKGPSPVFLAPLAPSSKSTSGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPV 180
Db 121 tvssastkgpsvflaplskskstsgtaalgclvkdyfpepvtvswnsgaltsgvhtfpav 180

QY 181 LQSSGLYSLSVVTPSPSSSLGTQTYICNVNHPKSNTKVDKKVEPKSCDKTHT 232
Db 181 lqssgylslssvvtvpssslgtqtyicnvnhkpsntkvdkkvepkscdktht 232

RESULT 14
AAR30774
ID AAR30774 standard; protein; 454 AA.
XX
AC AAR30774;
XX
DT 12-MAY-1993 (first entry)
XX
DE H52H4-160 murine anti-CD18 antibody heavy chain.
XX

```

```

XX Humanisation; rapid; monoclonal antibody.
XX
XX Mus musculus.
XX
PN WO9222653-A.
XX
PD 23-DEC-1992.
XX
XX 15-JUN-1992; 92WO-US05126.
XX
XX 14-JUN-1991; 91US-0715272.
XX
XX (GETH ) GENENTECH INC.
XX
XX Carter PJ, Presta LG;
XX
XX WPI; 1993-018139/02.
XX
XX Humanisation of antibodies - by molecular modelling of the variable
XX domains and alteration by gene conversion mutagenesis
XX
XX Disclosure; Fig 6A; 126pp; English.
XX
XX The sequence is that of the heavy chain of murine anti-CD18
XX antibody H52H4-160.
XX
XX Sequence 454 AA;
XX

Query Match 88.5%; Score 1091; DB 14; Length 454;
Best Local Similarity 85.8%; Pred. No. 9.8e-77;
Matches 199; Conservative 18; Mismatches 15; Indels 0; Gaps 0;

QY 1 EVLVESGGGLVOPGSLRLSCATSGYTFETMHWMRQAPGKGLWVAGINPKNGTSH 60
Db 1 evlqsggpelvkpgavskiscktsgytfttymhmksqshgkslewlgfnpknggssh 60

QY 61 NORFMDRFTISVDKSTSTAYMQMNSLRADTAVYYCARWRGLNYGDFVRYFDVWGOGTLV 120
Db 61 nqrfmdkatlavdkststaymelrsltsedsgiyycarwrglnygfdfvryfdvwgagttv 120

QY 121 TVSSASTKGPSPVFLAPLAPSSKSTSGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPV 180
Db 121 tvssastkgpsvflaplskskstsgtaalgclvkdyfpepvtvswnsgaltsgvhtfpav 180

QY 181 LQSSGLYSLSVVTPSPSSSLGTQTYICNVNHPKSNTKVDKKVEPKSCDKTHT 232
Db 181 lqssgylslssvvtvpssslgtqtyicnvnhkpsntkvdkkvepkscdktht 232

RESULT 15
AAY29444
ID AAY29444 standard; Protein; 253 AA.
XX
AC AAY29444;
XX
XX 05-OCT-1999 (first entry)
XX
XX Humanised anti-IL-8 6G4.2.5vll heavy chain and STII leader peptide.
XX
XX Antibody; humanised; anti-IL-8 monoclonal antibody; interleukin 8;
XX diagnosis; inflammatory disorder; conjugate; immunoglobulin;
XX fusion protein.
XX
XX Synthetic.
XX
XX Mus musculus.
XX
XX Homo sapiens.
XX
XX WO9937779-A1.
XX
XX 29-JUL-1999.
XX

```

```
PF 19-JAN-1999; 99WO-US01081.
XX
PR 24-JUL-1998; 98US-0122513.
PR 22-JAN-1998; 98US-0012116.
PR 20-FEB-1998; 98WO-US03337.
PR 24-JUL-1998; 98US-0121952.
XX
PA (GETH ) GENENTECH INC.
XX
XX Hsei V, Koumenis I, Leong SJ, Presta LG, Shahroksh Z;
PI Zapata GA;
XX
XX WPI; 1999-469134/39.
XX
PT New conjugates of nonproteinaceous polymers with antibody fragments,
PT used for treating inflammatory disorders
XX
PS Example; Fig 31; 36Opp; English.
XX
CC The present invention describes a novel conjugate having one or more
CC antibody fragments covalently attached to one or more nonproteinaceous
CC polymer molecules, where the apparent size of the conjugate is at least
CC about 500 kDa. Conjugates of antibody fragments which bind the human
CC interleukin (IL) 8 with a nonproteinaceous polymer can be used for
CC treating inflammatory disorders e.g. acute lung injury, ischaemic
CC reperfusion disorder, and autoimmune diseases. They can also be used
CC for treating e.g. inflammatory skin diseases including psoriasis and
CC atopic dermatitis, systemic scleroderma and sclerosis, and asthmatic
CC diseases. The conjugates can also be used as reagents in an animal
CC model system for in vivo study of the biological functions of the
CC antigen recognised by the conjugate. The present sequence represents
CC the humanised anti-IL-8 664.2.5 heavy chain in an N-terminal fusion
CC with the STII leader peptide from the present invention.
XX
SQ Sequence 253 AA;
```

Query Match 83.5%; Score 1030; DB 20; Length 253;
Best Local Similarity 84.0%; Pred. NO. 2.7e-72;
Matches 199; Conservative 12; Mismatches 14; Indels 12; Gaps 2;

```
QY 1 EVQLVESGGGLVQPGGSLRLSCATSGYTFEYTHMMROAPGKGLEWVAGINPKNGGTS 60
Db 24 evqlvqsgggivqp9gsirlscasgysfssymhwrqapkglewvgyiopsngetty 83
QY 61 NQRFMDRFTISVDKSTSTAYMQMNSLRAEDTAVYYCARWRGLNYGFDVRY-----EDVMG 115
Db 84 nqkfkgftrldnsnkntaylqmnsdraedtavyycarg-----dyryngdwffdvvg 136
QY 116 QGTLVTSSASTKGPSVTPPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVH 175
Db 137 qgtlvtvssastkgpsvfpplapssksts ggttaalgclvkdypfpvptvswngaltsgvh 196
QY 176 TFPVQLQSSGLYSLSVVTPVPSSSIGTQTYICNVNHPKSNKTKVDKKVEPKSCDKTHT 232
Db 197 tfpavlgssglyslssvvtpvpssslgtqtyicnvnhkpsntkvdkkvepkscdktht 253
```

Search completed: August 14, 2002, 11:00:45
Job time: 526 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 14, 2002, 10:57:15 ; Search time 20.83 seconds
(without alignments)
272.047 Million cell updates/sec

Title: US-09-811-384-10
Perfect score: 1233
Sequence: 1 EVQLVESGGGLVPGGSLRL.....PSNKTVDKVEPKSCDKTHT 232

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
- 2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
- 3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
- 4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
- 5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep.*
- 6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1233	100.0	232	2	US-07-934-373C-29
2	1233	100.0	232	2	US-08-788-800-10
3	1233	100.0	232	3	US-08-437-642B-29
4	1233	100.0	232	5	PCT-US93-07832-29
5	1233	100.0	235	2	US-07-934-373C-30
6	1233	100.0	235	3	US-08-437-642B-30
7	1233	100.0	235	5	PCT-US93-07832-30
8	1233	100.0	241	3	US-09-097-309-1
9	1233	100.0	241	4	US-09-097-171A-1
10	1233	100.0	300	3	US-09-097-309-7
11	1233	100.0	300	4	US-09-097-171A-11
12	1233	100.0	300	4	US-09-422-712B-3
13	1233	100.0	300	4	US-09-607-756-3
14	1216	98.6	232	2	US-07-934-373C-27
15	1216	98.6	232	3	US-08-437-642B-27
16	1216	98.6	232	5	PCT-US93-07832-27
17	1211	98.2	232	2	US-07-934-373C-28
18	1211	98.2	232	3	US-08-437-642B-28
19	1211	98.2	232	5	PCT-US93-07832-28
20	1207	97.9	232	2	US-07-934-373C-31
21	1207	97.9	232	2	US-07-934-373C-38
22	1207	97.9	232	3	US-08-437-642B-31
23	1207	97.9	232	3	US-08-437-642B-38
24	1207	97.9	232	5	PCT-US93-07832-31
25	1207	97.9	232	5	PCT-US93-07832-38
26	1206	97.8	232	2	US-07-934-373C-35
27	1206	97.8	232	2	US-07-934-373C-36

28	1206	97.8	232	3	US-08-437-642B-35	Sequence 35, Appl
29	1206	97.8	232	3	US-08-437-642B-36	Sequence 36, Appl
30	1206	97.8	232	5	PCT-US93-07832-35	Sequence 35, Appl
31	1206	97.8	232	5	PCT-US93-07832-36	Sequence 36, Appl
32	1205	97.7	232	2	US-07-934-373C-33	Sequence 33, Appl
33	1205	97.7	232	3	US-08-437-642B-33	Sequence 33, Appl
34	1205	97.7	232	5	PCT-US93-07832-33	Sequence 33, Appl
35	1198	97.2	232	2	US-07-934-373C-32	Sequence 32, Appl
36	1198	97.2	232	3	US-08-437-642B-32	Sequence 32, Appl
37	1198	97.2	232	5	PCT-US93-07832-32	Sequence 32, Appl
38	1195	96.9	232	2	US-07-934-373C-37	Sequence 37, Appl
39	1195	96.9	232	3	US-08-437-642B-37	Sequence 37, Appl
40	1195	96.9	232	5	PCT-US93-07832-37	Sequence 37, Appl
41	1191	96.6	232	2	US-07-934-373C-34	Sequence 34, Appl
42	1191	96.6	232	3	US-08-437-642B-34	Sequence 34, Appl
43	1191	96.6	232	5	PCT-US93-07832-34	Sequence 34, Appl
44	1171	95.0	232	2	US-07-934-373C-26	Sequence 26, Appl
45	1171	95.0	232	3	US-08-437-642B-26	Sequence 26, Appl

ALIGNMENTS

RESULT 1
US-07-934-373C-29
; Sequence 29, Application US/07934373C
; Patent No. 5821337
; GENERAL INFORMATION:
; APPLICANT: Paul J. Carter
; APPLICANT: Leonard G. Presta
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/934,373C
; FILING DATE: 21-Aug-1992
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/05126
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 232 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-07-934-373C-29

Query Match 100.0%; Score 1233; DB 2; Length 232;
Best Local Similarity 100.0%; Pred. No. 4.4e-100;
Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVOLVESGGLVQPGSLRLSCATSGYTFEYTMHMRQAPGKLEWVAGINPKNGTSH 60
Db 1 EVOLVESGGLVQPGSLRLSCATSGYTFEYTMHMRQAPGKLEWVAGINPKNGTSH 60
Qy 61 NORFMDRTTISVDKSTSTAYMQMNSLRADTAVYYCARWRGLNYGFDVRYFDVWGOGTLV 120
Db 61 NORFMDRTTISVDKSTSTAYMQMNSLRADTAVYYCARWRGLNYGFDVRYFDVWGOGTLV 120
Qy 121 TVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSKVHTFPV 180
Db 121 TVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSKVHTFPV 180
Qy 181 LQSSGLYSLSSVTVPPSSSLGTQTYICNVNHNKPSNTKVDKKEPKSCDKTHT 232
Db 181 LQSSGLYSLSSVTVPPSSSLGTQTYICNVNHNKPSNTKVDKKEPKSCDKTHT 232

RESULT 2
US-08-788-800-10
; Sequence 10, Application us/08788800
; Patent No. 5914112
; GENERAL INFORMATION:
; APPLICANT: Bednar, Martin M.
; APPLICANT: Thomas, G. Roger
; APPLICANT: Gross, Cordell E.
; TITLE OF INVENTION: ANTI-CD18 ANTIBODIES IN STROKE
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/788,800
; FILING DATE: 22-Jan-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0987r1
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 232 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-788-800-10

Query Match 100.0%; Score 1233; DB 2; Length 232;
Best Local Similarity 100.0%; Pred. No. 4.4e-100;
Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVOLVESGGLVQPGSLRLSCATSGYTFEYTMHMRQAPGKLEWVAGINPKNGTSH 60
Db 1 EVOLVESGGLVQPGSLRLSCATSGYTFEYTMHMRQAPGKLEWVAGINPKNGTSH 60
Qy 61 NORFMDRTTISVDKSTSTAYMQMNSLRADTAVYYCARWRGLNYGFDVRYFDVWGOGTLV 120
Db 61 NORFMDRTTISVDKSTSTAYMQMNSLRADTAVYYCARWRGLNYGFDVRYFDVWGOGTLV 120
Qy 121 TVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSKVHTFPV 180

Db 121 TVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSKVHTFPV 180
Qy 181 LQSSGLYSLSSVTVPPSSSLGTQTYICNVNHNKPSNTKVDKKEPKSCDKTHT 232
Db 181 LQSSGLYSLSSVTVPPSSSLGTQTYICNVNHNKPSNTKVDKKEPKSCDKTHT 232

RESULT 3
US-08-437-642B-29
; Sequence 29, Application US/08437642B
; Patent No. 6054297
; GENERAL INFORMATION:
; APPLICANT: Paul J. Carter
; APPLICANT: Leonard G. Presta
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/437,642B
; FILING DATE: 09-May-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/934373
; FILING DATE: 21-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/146206
; FILING DATE: 17-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/05126
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P2C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 232 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-437-642B-29

Query Match 100.0%; Score 1233; DB 3; Length 232;
Best Local Similarity 100.0%; Pred. No. 4.4e-100;
Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVOLVESGGLVQPGSLRLSCATSGYTFEYTMHMRQAPGKLEWVAGINPKNGTSH 60
Db 1 EVOLVESGGLVQPGSLRLSCATSGYTFEYTMHMRQAPGKLEWVAGINPKNGTSH 60
Qy 61 NORFMDRTTISVDKSTSTAYMQMNSLRADTAVYYCARWRGLNYGFDVRYFDVWGOGTLV 120
Db 61 NORFMDRTTISVDKSTSTAYMQMNSLRADTAVYYCARWRGLNYGFDVRYFDVWGOGTLV 120
Qy 121 TVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSKVHTFPV 180

Patent No. 6054297
; GENERAL INFORMATION:
; APPLICANT: Paul J. Carter
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/437,642B
; FILING DATE: 09-May-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/934373
; FILING DATE: 21-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/146206
; FILING DATE: 17-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/05126
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P2C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 235 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-437-642B-30

Query Match 100.0%; Score 1233; DB 3; Length 235;
Best Local Similarity 100.0%; Pred. No. 4.4e-100;
Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVQPGGSLRLSCATSGYTFETYMHWMRQAPGKGLWVAGINPKNGGTS 60
Db 1 EVQLVESGGGLVQPGGSLRLSCATSGYTFETYMHWMRQAPGKGLWVAGINPKNGGTS 60

QY 61 NQRFMDRTISVDKSTSTAYMQMNSLRAEDTAVYYCARWGLNYGFDVRYFDVWGQGLV 120
Db 61 NQRFMDRTISVDKSTSTAYMQMNSLRAEDTAVYYCARWGLNYGFDVRYFDVWGQGLV 120

QY 121 TVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYPPEPTVTSWNSGALTSGVHTFPAV 180
Db 121 TVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYPPEPTVTSWNSGALTSGVHTFPAV 180

QY 181 LQSSGLYSLSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHT 232
Db 181 LQSSGLYSLSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHT 232

RESULT 7
PCT-US93-07832-30
; Sequence 30, Application PC/TUS930782

; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/07832
; FILING DATE: 19930820
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/05126
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/934373
; FILING DATE: 21-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME:
; REGISTRATION NUMBER:
; REFERENCE/DOCKET NUMBER: 709P2PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE:
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 235 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
PCT-US93-07832-30

Query Match 100.0%; Score 1233; DB 5; Length 235;
Best Local Similarity 100.0%; Pred. No. 4.4e-100;
Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVQPGGSLRLSCATSGYTFETYMHWMRQAPGKGLWVAGINPKNGGTS 60
Db 1 EVQLVESGGGLVQPGGSLRLSCATSGYTFETYMHWMRQAPGKGLWVAGINPKNGGTS 60

QY 61 NQRFMDRTISVDKSTSTAYMQMNSLRAEDTAVYYCARWGLNYGFDVRYFDVWGQGLV 120
Db 61 NQRFMDRTISVDKSTSTAYMQMNSLRAEDTAVYYCARWGLNYGFDVRYFDVWGQGLV 120

QY 121 TVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYPPEPTVTSWNSGALTSGVHTFPAV 180
Db 121 TVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYPPEPTVTSWNSGALTSGVHTFPAV 180

QY 181 LQSSGLYSLSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHT 232
Db 181 LQSSGLYSLSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHT 232

RESULT 8
US-09-097-309-1
; Sequence 1, Application US/09097309
; Patent No. 6121428
; GENERAL INFORMATION:
; APPLICANT: Blank, Gregory S.
; APPLICANT: Narindray, Daljit S.


```

QY   121 TVSSASTKGPSVFPLAPSSKSTSGGTAALGLCLVCKDYFPEPVTYSWNSGALTSGVHTTFFAV 180
      |||||
Db    144 TVSSASTKGPSVFPLAPSSKSTSGGTAALGLCLVCKDYFPEPVTYSWNSGALTSGVHTTFFAV 203
      |||||

QY   181 LQSSGLYSLSSWVTPVPSSSFGTGTTYICNVNHNKPSNTKVDKKVEPKSCDKTKHT 232
      |||||
Db    204 LQSSGLYSLSSWVTPVPSSSFGTGTTYICNVNHNKPSNTKVDKKVEPKSCDKTKHT 255
      |||||

RESULT 13
US-09-607-756-3
; Sequence 3, Application US/09607756
; Patent No. 6258560
; GENERAL INFORMATION:
; APPLICANT: Leung, Woon-Lam Susan
; APPLICANT: Swartz, James R.
; TITLE OF INVENTION: PROCESS FOR BACTERIAL PRODUCTION OF POLYPEPTIDES
; FILE REFERENCE: P1711R1
; CURRENT APPLICATION NUMBER: US/09/607,756
; CURRENT FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: US 09/422,712
; PRIOR FILING DATE: 1999-10-21
; NUMBER OF SEQ ID NOS: 4
; SEQ ID NO 3
; LENGTH: 300
; TYPE: PRT
; ORGANISM: Human
US-09-607-756-3
```

```

; APPLICATION NUMBER: US/07/934/373C
; FILING DATE: 21-AUG-1992
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/05126
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 232 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-07-934-373C-27

Query Match 98.6%; Score 1216; DB
Best Local Similarity 98.3%; Pred. No. 1.3e-
Matches 228; Conservative 2; Mismatches

QY 1 EVLVESGGGLVQPGGSLRLSCATSGYTFEYTMHWNRQ
DB 1 EVLVESGGGLVQPGGSLRLSCATSGYTFEYTMHWNRQ
QY 61 NQRFMDRFTISVDKSTSTAYMQNSLRAEDTAVYVCARW
DB 61 NQRFMDRFTISVDKSKNTLYLQNSLRAEDTAVYVCARW
QY 121 TVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPE
DB 121 TVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPE
QY 181 LOSGGLYSLSSVTVFVPSSSLGTQTYICNVNHHKPSNTKVDI
DB 181 LOSGGLYSLSSVTVFVPSSSLGTQTYICNVNHHKPSNTKVDI

RESULT 15
US-08-437-642B-27
; Sequence 27, Application US/08437642B
; Patent No. 6054297
; GENERAL INFORMATION:
; APPLICANT: Paul J. Carter
; APPLICANT: Leonard G. Presta
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/437,642B
; FILING DATE: 09-May-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/934373
; FILING DATE: 21-AUG-1992

```

;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/146206
;; FILING DATE: 17-NOV-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US92/05126
;; FILING DATE: 15-JUN-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/115272
;; FILING DATE: 14-JUN-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Lee, Wendy M.
;; REGISTRATION NUMBER: 40,378
;; REFERENCE/DOCKET NUMBER: P0709P2C1
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 650/225-1994
;; TELEFAX: 650/952-9881
;; INFORMATION FOR SEQ ID NO: 27:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 232 amino acids
;; TYPE: Amino Acid
;; TOPOLOGY: Linear
US-08-437-642B-27

Query Match 98.6%; Score 1216; DB 3; Length 232;
Best Local Similarity 98.3%; Pred. No. 1.3e-98;
Matches 228; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
Qy 1 EVQLVESGGGLVQPGGSLRLSCATSGYTFEYTMHWNRQAPGKLEWVAGINPKNGGTSH 60
Db 1 EVQLVESGGGLVQPGGSLRLSCATSGYTFEYTMHWNRQAPGKLEWVAGINPKNGGTSH 60
Qy 61 NQRFMDRFTISVDKSTSTAYMQMNSLRAEDTAVYYCARWRGLNYGFDVRYFDVWGQGLV 120
Db 61 NQRFMDRFTISVDKSKNTLYLQMNLSLRAEDTAVYYCARWRGLNYGFDVRYFDVWGQGLV 120
Qy 121 TVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV 180
Db 121 TVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV 180
Qy 181 LQSSGLYSLSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHT 232
Db 181 LQSSGLYSLSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHT 232

Search completed: August 14, 2002, 11:01:12
Job time: 237 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 14, 2002, 11:05:26 ; Search time 29.5 Seconds
(without alignments)
697.055 Million cell updates/sec

Title: US-09-811-384-11
Perfect score: 1118
Sequence: 1 DIQMTQSPSSLSASVGRVT.....EVTHQGLSSPVTKSFNRGEC 214

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues
Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	938.5	83.9	215	2 JE0244	Ig kappa chain NIG
2	934.5	83.6	215	2 JE0242	Ig kappa chain NIG
3	916.5	82.0	215	2 JE0243	Ig kappa chain NIG
4	869.5	77.8	215	2 A23746	Ig kappa chain V-I
5	843	75.4	216	2 JE0241	Ig kappa chain Am3
6	758	67.8	230	2 S33161	Ig kappa chain - s
7	736	65.8	234	2 S14237	Ig kappa chain pre
8	735	65.7	240	2 S06084	Ig kappa chain pre
9	718	64.2	220	2 A31790	Ig kappa chain V r
10	717	64.1	234	2 S01320	Ig kappa chain pre
11	707.5	63.3	219	2 S52028	Ig kappa chain - m
12	703	62.9	218	2 S68241	Ig kappa chain V r
13	701	62.7	218	2 JC5810	monoclonal antibod
14	700.5	62.7	219	2 PC4203	Ig kappa chain (mo
15	697.5	62.4	225	2 S37484	Ig kappa chain - m
16	694	62.1	214	2 S68212	Ig kappa chain (Ma
17	693.5	62.0	219	2 S38865	Ig kappa chain - m
18	691.5	61.9	217	2 S42772	Ig kappa chain - m
19	684.5	61.2	235	2 S25058	Ig kappa chain - m
20	680.5	60.9	219	2 S16112	Ig kappa chain V r
21	669	59.8	210	2 A56169	Ig kappa chain V r
22	667.5	59.7	225	2 JL0029	Ig kappa chain pre
23	612.5	54.8	135	2 S52059	JC-kappa protein -
24	586	52.4	178	2 PT0219	Ig kappa chain V-C
25	581.5	52.0	229	2 A20969	Ig kappa chain pre
26	548	49.0	106	1 K3HU	Ig kappa chain C r
27	528.5	47.3	238	2 A49633	Ig lambda-like cha
28	513	45.9	99	2 A37927	Ig kappa chain C r
29	507	45.3	99	2 S26653	Ig kappa chain C r

30	506.5	45.3	197	2 S29593	Ig kappa chain (WM
31	499	44.6	127	2 S40367	Ig kappa chain V-J
32	496	44.4	139	2 S40365	Ig kappa chain - h
33	491	43.9	141	2 A49134	Ig kappa chain V-I
34	487	43.6	123	2 S40331	Ig kappa chain - h
35	484	43.3	108	2 B49047	Ig kappa chain V r
36	484	43.3	131	2 S40352	Ig kappa chain V-J
37	482	43.1	122	2 S40314	Ig kappa chain - h
38	481	43.0	132	2 S40334	Ig kappa chain - h
39	480	42.9	108	2 S19674	Ig kappa chain V r
40	476.5	42.6	124	2 S40336	Ig kappa chain V-J
41	476	42.6	144	2 PL0106	Ig kappa chain pre
42	475	42.5	109	2 S31981	Ig kappa chain - h
43	474	42.4	108	1 KJHULY	Ig kappa chain V-I
44	474	42.4	130	2 S40368	Ig kappa chain - h
45	473	42.3	129	2 S40317	Ig kappa chain - h

ALIGNMENTS

RESULT 1
JE0244
Ig kappa chain NIG2 precursor - human
C:Species: Homo sapiens (man)
C:Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C:Accession: JE0244
R:Alim, M.A.; Hara, Y.; Hossain, M.S.; Takeda, K.; Yamagata, F.; Yamaki, S.; Kazi, H.
submitted to JIPID, November 1998
A:Description: A new subgroup of k type light chains (VKV) identified in cases of AL
A:Reference number: JE0243
A:Accession: JE0244
A:Molecule type: protein
A:Residues: 1-215 <ALI>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 83.9%; Score 938.5; DB 2: Length 215;
Best Local Similarity 83.7%; Pred. No. 1.4e-55;
Matches 180; Conservative 17; Mismatches 1; Gaps 1;

Qy	1	DIQMTQSPSSLSASVGRVTITCRASQDINNYLNWYQKPGKAPKLLIYYTSLHSGVPS	60
Db	1	EVLTQSPATLSVSPGERATLSCRASQSVHSLAWYQKPGQAPRLLIYRASTRATGIPA	60
Qy	61	RFGSGSGTDYTLTISSLPEDFATYYCOQGNLPP-TEGQGTKEIKRTVAAPSVFIEP	119
Db	61	RFGSGSGTDFTLTITSSQSEDFALYYCOQYNTWPLTEGGGTKEIKRTVAAPSVFIEP	120
Qy	120	PSDEQLKSGTASVWCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSSTLSSTL	179
Db	121	PSDEQLKSGTASVWCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSSTLSSTL	180
Qy	180	TLSKADYEKKHYACEVTHQGLSSPVTKSFNRGEC	214
Db	181	TLSKADYEKKHYACEVTHQGLSSPVTKSFNRGEC	215

RESULT 2
JE0242
Ig kappa chain NIG26 precursor - human
C:Species: Homo sapiens (man)
C:Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C:Accession: JE0242
R:Alim, M.A.; Yamaki, S.; Hossain, M.S.; Takeda, K.; Kojima, M.; Takashi, I.; Shinoda
submitted to JIPID, November 1998
A:Description: Structure relationship of kappa type light chains with AL amyloidosis:
A:Reference number: JE0241
A:Accession: JE0242
A:Molecule type: protein
A:Residues: 1-215 <ALI>
C:Superfamily: immunoglobulin V region; immunoglobulin homology


```
Db 61 ESGVDRFTSGSGTDTFTLTSSVQAEADLAVYYCONDYSNLPTFGGGTKLELKRADAAPT 120
QY 115 VFIPPPDEQLKSGTASVYVCLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYSTS 174
    ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 121 VSIFPPSSSEQLTSGGASVVCFLNFPKPDINVKWKIDGSRQNGVLSWTDQDSKDSYSTS 180
QY 175 LSSTLTLSKADYEKKHYACEVTHQGLSSPVTKSFNRGEC 214
    :|||||: | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 181 MSSTLTLTQDEYERHNSYTCETHKTSTSPIVKSFNRNEC 220
    :|||||: | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|

RESULT 10
S01320
Ig kappa chain precursor - mouse
C:Species: Mus musculus (house mouse)
C>Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 21-Jan-2000
C:Accession: S01320
R:de Waele, P.; Feys, V.; van de Voorde, A.; Molemans, F.; Fliers, W.
Eur. J. Biochem. 176, 287-295, 1988
A:Title: Expression in non-lymphoid cells of mouse recombinant immunoglobulin directed a
A:Reference number: S01320; MUID:88329081
A:Accession: S01320
A:Molecule type: mRNA
A:Residues: 1-234 <DE1>
A:Cross-references: EMBL:X13187; NID:g51784; PIDN:CAA31579.1; PID:g51785
A:Note: this sequence was determined from the differentiated gene
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-234/Product: Ig kappa chain #status predicted <MAT>
F:36-110/Domain: immunoglobulin homology <IMM>

Query Match 64.1%; Score 717; DB 2; Length 234;
Best Local Similarity 63.6%; Pred. No. 7.6e-41;
Matches 136; Conservative 29; Mismatches 49; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVITTCRASQDINNLYNWYQKPGKAPKLLIYYTSTLHS 60
    ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 21 DIQMTQSPASLSVSGESVITTCRASQDINNLYNWYQKPGKAPKLLIYYTSTLHS 80
QY 61 RFSGSGSGTDYTLTISSLPQEDFATYYCOQGNLTPPTFGQGTKEIKRTVAAPS 120
    ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 81 RFSGSGSGTDYTLTISSLPQEDFATYYCOQGNLTPPTFGQGTKEIKRTVAAPS 140
QY 121 SDQLKSGTASVYVCLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYSTS 180
    ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 141 SSELTSGGASVVCFLNFPKPDINVKWKIDGSRQNGVLSWTDQDSKDSYSTS 200
QY 181 LSKADYEKKHYACEVTHQGLSSPVTKSFNRGEC 214
    || :||: | || | :||: ||||| ||
Db 201 LTRDEYERHNSYTCETHKTSTSPIVKSFNRNEC 234

RESULT 11
S52028
Ig kappa chain - mouse
C:Species: Mus musculus (house mouse)
C>Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
C:Accession: S52028
R:van Engelen, F.; Schouten, A.; Molthoff, J.W.; Roosien, J.; Dirkse, W.G.; Schots, A.;
submitted to the EMBL Data Library, August 1994
A:Description: Coordinate expression of antibody subunit genes yields high levels of fur
A:Reference number: S52028
A:Accession: S52028
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-219 <VAN>
A:Cross-references: EMBL:L35138; NID:g522336; PIDN:AAA67525.1; PID:g522337
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:16-95/Domain: immunoglobulin homology <IMM>
```

```
Query Match 63.3%; Score 707.5; DB 2; Length 219;
Best Local Similarity 60.7%; Pred. No. 3e-40;
Matches 133; Conservative 29; Mismatches 52; Indels 5; Gaps 1;

QY 1 DIQMTQSPSSLSASVGRVITTCRASQDINNLYNWYQKPGKAPKLLIYYTSTLH 55
    ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 DVMVTQSPSLPVSIGDQASISCRSQSIHVSNGNTYLEMYLQKPGSKLLIYKVS 60
QY 56 SGVPSRFSGSGGTDTLTITSSLPQEDFATYYCOQGNLTPPTFGQGTKEIKRTVAAPS 115
    ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 61 SGVPSRFSGSGGTDTLTITSSLPQEDFATYYCOQGNLTPPTFGQGTKEIKRTVAAPS 120
QY 116 FIFPPSDEQLKSGTASVYVCLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYSTS 175
    ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 121 SIFPPSDEQLTSGGASVVCFLNFPKPDINVKWKIDGSRQNGVLSWTDQDSKDSYSTS 180
QY 176 SFTLTLKADYEKKHYACEVTHQGLSSPVTKSFNRGEC 214
    ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 181 SFTLTLKADYEKKHYACEVTHQGLSSPVTKSFNRGEC 219
    ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 12
S68241
Ig kappa chain V region (Mab13-1) - mouse (fragment)
N:Alternate names: immunoglobulin light chain
C:Species: Mus musculus (house mouse)
C>Date: 24-Aug-1996 #sequence_revision 13-Mar-1997 #text_change 20-Jun-2000
C:Accession: S68241; S68214
R:Takagi, M.; Kohda, K.; Hamuro, T.; Harada, A.; Yamaguchi, H.; Kamachi, M.; Inanaka,
submitted to the EMBL Data Library, March 1994
A:Description: Specific peroxidase activity by formation of an antibody L-chain-porphyr
A:Reference number: S68241
A:Accession: S68241
A:Molecule type: mRNA
A:Residues: 1-218 <TAK>
A:Cross-references: EMBL:D29670; NID:g473962; PIDN:BAA06141.1; PID:g473963
R:Takagi, M.; Kohda, K.; Hamuro, T.; Harada, A.; Yamaguchi, H.; Kamachi, M.; Inanaka,
PDBS Lett. 375, 273-276, 1995
A:Title: Thermostable peroxidase activity with a recombinant antibody L chain-porphyr
A:Reference number: S68211; MUID:96085223
A:Accession: S68214
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 'N1', 3-212 <TAW>
A:Cross-references: EMBL:D29670
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin

Query Match 62.9%; Score 703; DB 2; Length 218;
Best Local Similarity 59.6%; Pred. No. 6e-40;
Matches 130; Conservative 35; Mismatches 49; Indels 4; Gaps 1;

QY 1 DIQMTQSPSSLSASVGRVITTCRASQDINNLYNWYQKPGKAPKLLIYYTSTLH 56
    :: :|||: || :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 1 ELVLTQSPASLAVSLGQRATISCRASKSVASGYIYHWNVYQKPGKAPKLLISLATNLES 60
QY 57 GVPSPRFSGSGGTDTLTITSSLPQEDFATYYCOQGNLTPPTFGQGTKEIKRTVAAPS 116
    ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 61 GVPSPRFSGSGGTDTLTITSSLPQEDFATYYCOQGNLTPPTFGQGTKEIKRTVAAPS 120
QY 117 FIFPPSDEQLKSGTASVYVCLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYSTS 176
    ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 121 FIFPPSDEQLTSGGASVVCFLNFPKPDINVKWKIDGSRQNGVLSWTDQDSKDSYSTS 180
QY 177 SFTLTLKADYEKKHYACEVTHQGLSSPVTKSFNRGEC 214
    ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 181 SFTLTLKADYEKKHYACEVTHQGLSSPVTKSFNRGEC 218
    ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 13
JC5810
```


monoclonal antibody 13-1 light chain - mouse

C:Species: Mus musculus (house mouse)

C>Date: 04-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 21-Jan-2000

C:Accession: JCS810

R:Akashi, S.; Kato, K.; Torizawa, T.; Dohmae, N.; Yamaguchi, H.; Kamachi, M.; Harada, A.

Biochem. Biophys. Res. Commun. 240, 566-572, 1997

A:Title: Structural characterization of mouse monoclonal antibody 13-1 against a porphyrin

A:Reference number: JCS810; MUID:98063277

A:Accession: JCS810

A:Molecule type: protein

A:Residues: 1-218 <AKA>

C:Comment: This catalytic antibody has peroxidase oxidase. It is directed against a porphyrin

C:Superfamily: immunoglobulin V region; immunoglobulin homology

F:16-94/Domain: immunoglobulin homology <IMM>

Query Match 62.7%; Score 701; DB 2; Length 218;

Best Local Similarity 60.1%; Pred. No. 8.2e-40;

Matches 131; Conservative 33; Mismatches 50; Indels 4; Gaps 1;

QY 1 DIQMTQSPSSLSASVGRVTITCRASQDINN----YLNWYQKPGKAPKLLIYYTSTLHS 56

DB 1 NIVLTQSPASLASVLSGORATISCRASKSVSASGYIMHWYQKPGQPKLLISLNSLES 60

QY 57 GVPSPRSFGSGSDYTLTISSLOPEDFATYYCOQGNLTLPPTFGQGTKEIKRTVAAPSVF 116

DB 61 GVPARESGSGSDYTLNTHPVEEDVATYYCOHRELPLTFGAGTKLEKRAADAAPTVS 120

QY 117 IFPPSPDEQLKSGTASVCLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYSL 176

DB 121 IFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSRQNGVLNWTQDQSKDSTYSMS 180

QY 177 STLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 214

DB 181 STLTLTKEVERHNSYTCETHKTSPIVKSFNRNEC 218

RESULT 14

PC4203

Ig kappa chain (monoclonal antibody Maba34) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 31-Dec-1996 #sequence_revision 31-Dec-1996 #text_change 11-Jan-2000

C:Accession: PC4203

R:Kwak, J.W.; Lee, D.I.; Choi, B.K.; Cho, W.K.; Lee, S.H.; Park, Y.B.; Han, M.H.

Gene 173, 257-259, 1996

A:Title: Cloning and characterization of cDNAs coding for heavy and light chains of a monoclonal antibody

A:Reference number: PC4202; MUID:97082978

A:Accession: PC4203

A:Molecule type: mRNA

A:Residues: 1-219 <KWA>

C:Cross-references: GB:U29147; NID:g1594225; PIDN:AA52821.1; PID:g1594226

C:Comment: This protein is specific for human plasma apolipoprotein A-I of high-density

C:Superfamily: immunoglobulin V region; immunoglobulin homology

F:1-112/Domain: V region #status predicted <VRG>

F:113-219/Domain: C region #status predicted <CRG>

Query Match 62.7%; Score 700.5; DB 2; Length 219;

Best Local Similarity 60.3%; Pred. No. 8.9e-40;

Matches 132; Conservative 30; Mismatches 52; Indels 5; Gaps 1;

QY 1 DIQMTQSPSSLSASVGRVTITCRASQDI-----NNYLNWYQKPGKAPKLLIYYTSTLH 55

DB 1 DVLMTQTLPLSPVSLGDAQASISCRSSQSIHTNGNTVLEWYLOKPGQSPKLLIYKVSNR 60

QY 56 SGVPSRFSFGSGSDYTLTISSLOPEDFATYYCOQGNLTLPPTFGQGTKEIKRTVAAPS 115

DB 61 SGVPSRFSFGSGSDYTLTISSLOPEDFATYYCOQGNLTLPPTFGQGTKEIKRTVAAPS 120

QY 116 FTTPPSDEQLKSGTASVCLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYSL 175

DB 121 STFPSPSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSRQNGVLNWTQDQSKDSTYS 180

QY 176 SSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 214

DB 181 SSTLTLTKEVERHNSYTCETHKTSPIVKSFNRNEC 219

RESULT 15

S37484

Ig kappa chain - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 11-Jan-2000

C:Accession: S37484

R:Ducancel, F.F.D.

Submitted to the EMBL Data Library, February 1993

A:Reference number: S37483

A:Accession: S37484

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-225 <DUG>

A:Cross-references: EMBL:X70424; NID:g406254; PIDN:CAA49869.1; PID:g406255

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

Query Match 62.4%; Score 697.5; DB 2; Length 225;

Best Local Similarity 61.5%; Pred. No. 1.4e-39;

Matches 131; Conservative 32; Mismatches 49; Indels 1; Gaps 1;

QY 2 IQMTQSPSSLSASVGRVTITCRASQDINNYLNWYQKPGKAPKLLIYYTSTLHGVPSR 61

DB 14 IVMTQTPKFLLLSAGDRVTITCKASQSVSNVAVYQKPGQSPKLLIYVASSRYTGVDPDR 73

QY 62 FSGSGSGTDYTLTISSLOPEDFATYYCOQGNLTLPPTFGQGTKEIKRTVAAPSFIFFPS 121

DB 74 FTGSGYGTDTFTISTVQAEDLAVYFCQDYS-SYTFGGGTKEIKRAADAAPTIVSIFPPS 132

QY 122 DEQLKSGTASVCLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYSLSTLTFL 181

DB 133 SEQLTSGGASVVCFLNNFYPKDINVKWKIDGSRQNGVLNWTQDQSKDSTYSMSSTLTFL 192

QY 182 SKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 214

DB 193 TKDEVERHNSYTCETHKTSPIVKSFNRNEC 225

Search completed: August 14, 2002, 11:05:26

Job time: 361 sec


```
RL Hoppe-Seyler's Z. Physiol. Chem. 348:1718-1722(1967).
RN [7]
RP SEQUENCE (BENCE-JONES PROTEIN AG).
RX MEDLINE=69234734; PubMed=4893682;
RA Titani K., Shinoda T., Putnam F.W.;
RT "The amino acid sequence of a kappa type Bence-Jones protein. 3. The
RT complete sequence and the location of the disulfide bridges.";
RL J. Biol. Chem. 244:3550-3560(1969).
RN [8]
RP SEQUENCE (WALDENSTROM'S MACROGLOBULIN OU).
RX MEDLINE=70201507; PubMed=5447531;
RA Kohler H., Shimizu A., Paul C., Putnam F.W.;
RT "Macroglobulin structure: variable sequence of light and heavy
RT chains.";
RL Science 169:56-59(1970).
CC -!- MISCELLANEOUS: THE EU SEQUENCE HAS THE INV (3) ALLOTYPIC MARKER,
CC 45-ALA & 83-VAL. THE ROY SEQUENCE HAS THE INV (1,2) ALLOTYPIC
CC MARKER, 45-ALA AND 83-LEU.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; J00241; AAA58989.1; -
DR EMBL; V00557; CAA23823.1; -
DR PIR; A02116; K3HU.
DR HSP; P01842; 7FAB.
DR MIM; 147200; -
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_c1.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00407; Igcl; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1
FT DISULFID 26 86
FT VARIANT 83 83
FT INTERCHAIN (WITH A HEAVY CHAIN).
FT V -> L (IN INV(1,2) MARKER).
FT /FTIQ-VAR_003897.
FT DISULFID 14 14
FT D -> N (IN REF. 7 AND 8).
FT CONFLICT 57 57
FT E -> O (IN REF. 5 AND 6).
FT CONFLICT 57 57
SQ SEQUENCE 106 AA; 11609 MW; 51984D1FDD372CE8 CRC64;

Query Match 49.0%; Score 548; DB 1; Length 106;
Best Local Similarity 100.0%; Pred. No. 7.8e-39;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 109 TAAAPSVIFPPSDQLKSGTASVCLLNFPYREAKVQKVDNALQSGNSQESVTEQDS 168
Db 1 TAAAPSVIFPPSDQLKSGTASVCLLNFPYREAKVQKVDNALQSGNSQESVTEQDS 60
QY 169 KDSTYSLSSTLTSLKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 214
Db 61 KDSTYSLSSTLTSLKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 106

RESULT 2
KV1M_HUMAN
ID KV1M_HUMAN STANDARD; PRT; 108 AA.
AC P01605;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Lay.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;

Query Match 49.0%; Score 548; DB 1; Length 106;
Best Local Similarity 100.0%; Pred. No. 7.8e-39;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 109 TAAAPSVIFPPSDQLKSGTASVCLLNFPYREAKVQKVDNALQSGNSQESVTEQDS 168
Db 1 TAAAPSVIFPPSDQLKSGTASVCLLNFPYREAKVQKVDNALQSGNSQESVTEQDS 60
QY 169 KDSTYSLSSTLTSLKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 214
Db 61 KDSTYSLSSTLTSLKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 106
```

```

RN [1]
RP SEQUENCE.
RX MEDLINE=77038198; PubMed=824717;
RA Capra J.D., Klapper D.G.;
RT "Complete amino acid sequence of the variable domains of two human
RT IgM anti-gamma globulins (Lay/Pom) with shared idiotypic
RT specificities.";
RL Scand. J. Immunol. 5:677-684(1976).
CC -!- MISCELLANEOUS: THE SECOND AND THIRD HYPERVARIABLE REGIONS OF THIS
CC CHAIN ARE IDENTICAL WITH THOSE OF THE HUMAN POM V-III KAPPA CHAIN,
CC WITH WHICH IT SHARES CERTAIN IDIOTYPIC DETERMINANTS.
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA
CC GLOBULIN ACTIVITY.
DR PIR; A01871; K1HULY.
DR HSP; P01607; IREI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 34
FT DOMAIN 35 49
FT DOMAIN 50 56
FT DOMAIN 57 88
FT DOMAIN 89 97
FT DOMAIN 98 107
FT DISULFID 23 88
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11834 MW; 739993A95431434A CRC64;

Query Match 42.4%; Score 474; DB 1; Length 108;
Best Local Similarity 83.3%; Pred. No. 1e-32;
Matches 90; Conservative 6; Mismatches 12; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCRASQDINNLYNNYQKPKAPKLLIYYTSLHSGVPS 60
Db 1 DIQMTQSPSSLSVSGDRVTITCQASQNVNAYLNWYQKPKGLAKLLIYGASTREAGVPS 60
QY 61 RFGSGSGTDTLTITSSLOPEDFATYYCQGNLPTPTFGQGTKEVTKR 108
Db 61 RFGSGSGTDTFTTITSSLOPEDATYYCQYNNWPPPTFGQGTKEVTKR 108

RESULT 3
KV1H_HUMAN
ID KV1H_HUMAN STANDARD; PRT; 108 AA.
AC P01600;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Hau.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=71032830; PubMed=4097974;
RA Watanabe S., Hilschmann N.;
RT "The primary structure of a monoclonal kappa-type immunoglobulin L-
RT chain of subgroup I (Bence-Jones Protein Hau): subdivision within
RT subgroups.";
RL Hoppe-Seyler's Z. Physiol. Chem. 351:1291-1295(1970).
CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR PIR; A01868; K1HUHU.
DR HSP; P80362; 1WTL.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
```

KW Immunoglobulin V region; Bence-Jones protein.

```
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 107 FRAMEWORK-4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11671 MW; 08D3A6160BD0618 CRC64;
```

Query Match 42.0%; Score 470; DB 1; Length 108;
Best Local Similarity 83.3%; Pred. No. 2.2e-32;
Matches 90; Conservative 9; Mismatches 9; Indels 0; Gaps 0;

```
Qy 1 DIQMTQSPSSLSASVGDRTVITCRASQDINNLYNWYQKPGKAPKLLIYYTSTLHSGVPS 60
Db 1 DIQMTQSPSSLSASVGDRTVITCRASQSSYLSWYQKPGKAPQVLIYRASSLPVSGVPS 60

Qy 61 RFSGSGSGTDYTLTISSLOPEDFATYYCQGNLTPPTFGQGTKEIKR 108
Db 61 RFSGSGSGTDFTLTISLQPEDFATYYCQNYITPFSFGQGTVEIKR 108
```

RESULT 4

```
ID KV5Q_MOUSE STANDARD; PRT; 108 AA.
AC P01648;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-V region HP 91A3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RC STRAIN=A/J;
RX MEDLINE=82150934; PubMed=6801658;
RA Siegelman M., Capra J.D.;
RT "Complete amino acid sequence of light chain variable regions derived
RT from five monoclonal anti-p-azophenylarsenate antibodies differing
RT with respect to a crossreactive idiotype."
RL Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).
CC -!- MISCELLANEOUS: ANTI-ARSONATE HYBRIDOMA PROTEIN.
DR PIR: A01927; KMSAR.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
KW Immunoglobulin V region; Antiarsenate antibody.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 108 FRAMEWORK-4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11961 MW; D52EDA5E9A45291C CRC64;
```

Query Match 41.9%; Score 468; DB 1; Length 108;
Best Local Similarity 81.5%; Pred. No. 3.2e-32;
Matches 88; Conservative 10; Mismatches 10; Indels 0; Gaps 0;

```
Qy 1 DIQMTQSPSSLSASVGDRTVITCRASQDINNLYNWYQKPGKAPKLLIYYTSTLHSGVPS 60
Db 1 DIQMTQSPSSLSASLGDRTVITCRASQDINNLYNWYRQKPDGTGVTKLLIYYTSRLHSGVPS 60
```

```
Qy 61 RFSGSGSGTDYTLTISSLOPEDFATYYCQGNLTPPTFGQGTKEIKR 108
Db 61 RFSGSGSGTDYSLTISNLEQEDISTYFCQGNALPRTFGGKTKEIKR 108
```

RESULT 5

```
KV1Y_HUMAN STANDARD; PRT; 108 AA.
ID KV1Y_HUMAN
AC P80362;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region WAT.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE, AND X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RX MEDLINE=95086080; PubMed=7993911;
RX Huang D.-B., Chang C.-H., Ainsworth C., Bruenger A.T., Eulitz M.,
RX Solomon A., Stevens F.J., Schiffer M.;
RT "Comparison of crystal structures of two homologous proteins:
RT structural origin of altered domain interactions in immunoglobulin
RT light-chain dimers."
RL Biochemistry 33:14848-14857(1994).
RN [2]
RP SEQUENCE OF 1-35.
RX MEDLINE=81267384; PubMed=6167731;
RX Stevens F.J., Westholm F.A., Panagiotopoulos N., Schiffer M.,
RX Popp R.A., Solomon A.;
RT "Characterization and preliminary crystallographic data on the VL-
RT related fragment of the human kappa Bence Jones protein Wat."
J. Mol. Biol. 147:185-193(1981).
CC -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR PDB; 1WTL; 01-NOV-94.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
KW Immunoglobulin V region; Bence-Jones protein; 3D-structure.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 107 FRAMEWORK-4.
FT DISULFID 23 88 BY SIMILARITY.
FT CONFLICT 30 31 TN -> SD (IN REF. 2).
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11737 MW; D9D941B3F0FAE697 CRC64;
```

Query Match 41.8%; Score 467; DB 1; Length 108;
Best Local Similarity 82.4%; Pred. No. 3.8e-32;
Matches 89; Conservative 9; Mismatches 10; Indels 0; Gaps 0;

```
Qy 1 DIQMTQSPSSLSASVGDRTVITCRASQDINNLYNWYQKPGKAPKLLIYYTSTLHSGVPS 60
Db 1 DIQMTQSPSSLSASVGDRTVITCRASQDITNVNMFQRPQGPQKVLIIYGASILETGVP 60

Qy 61 RFSGSGSGTDYTLTISSLOPEDFATYYCQGNLTPPTFGQGTKEIKR 108
Db 61 RFSGSGSGTDFTLTISLQPEDIATYYCQYDTLPLTEGGGKTVDIKR 108
```

RESULT 6

```
KV1B_HUMAN STANDARD; PRT; 108 AA.
ID KV1B_HUMAN
AC P01594;
DT 21-JUL-1986 (Rel. 01, Created)
```

```

DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE Ig kappa chain V-I region AU.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=72189444; PubMed=5028201;
RA Schiechl H., Hilschmann N.;
RT "Rule of antibody structure. The primary structure of a monoclonal
RT immunoglobulin L-chain of the kappa-type, subgroup I (Bence-Jones
RT protein Au).";
RL Hoppe-Seyler's Z. Physiol. Chem. 353:345-370(1972).
RN [2]
RP X-RAY CRYSTALLOGRAPHY.
RX MEDLINE=77022433; PubMed=1234024;
RA Fehlgammer H., Schiffer M., Epp O., Colman P.M., Lattman E.E.,
RA Schwager P., Steigemann W., Schramm H.J.;
RT "The structure determination of the variable portion of the
RT Bence-Jones protein Au.";
RL Biophys. Struct. Mech. 1:139-146(1975).
CC -!- MISCELLANEOUS: THE STRUCTURE OF THE V REGION WAS DETERMINED BY
CC MOLECULAR REPLACEMENT METHODS USING THE KNOWN STRUCTURE OF THE V
CC REGION OF THE KAPPA CHAIN REI.
CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC PIR: A01862; K1HUAU.
DR HSP; P01607; 1REI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 FRAMEWORK-4.
FT DOMAIN 98 107 COMPLEMENTARITY-DETERMINING-3.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11939 MW; E8011187EB6F6PB9 CRC64;

Query Match 41.7%; Score 466; DB 1; Length 108;
Best Local Similarity 84.3%; Pred. No. 4.7e-32;
Matches 91; Conservative 5; Mismatches 12; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVTITCRASQDINNNYLNWYQOKPGKAPKLLIYVSTLHSGVPS 60
Db 1 DIQMTQSPSSLSASVGRVTITCRASQDINNNYLNWYQOKPGKAPKLLIYDASNLSESGVPS 60

Qy 61 RFSGSGSGDYTLTITSSLOPEDFATYCCQGNLPTPTFGGKTVEIKR 108
Db 61 RFSGSGSGAHFTTITSSLOPEDATYCCQYDYLPTWTFGGKTVEIKR 108

RESULT 7
KV5N_MOUSE
ID KV5N_MOUSE STANDARD; PRT; 108 AA.
AC P01647;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE Ig kappa chain V-V region HP 124E1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]

```

```

RP SEQUENCE.
RX STRAIN=A/J;
RX MEDLINE=82150934; PubMed=6801658;
RA Siegelman M., Capra J.D.;
RT "Complete amino acid sequence of light chain variable regions derived
RT from five monoclonal anti-p-azophenylarsenate antibodies differing
RT with respect to a crossreactive idiotype.";
RL Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).
CC -!- MISCELLANEOUS: ANTI-ARSONATE HYBRIDOMA PROTEIN.
DR PIR: A01927; KVMSAR.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Antiarsenate antibody.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 108 FRAMEWORK-4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11965 MW; 39971BC653EFEFA2 CRC64;

Query Match 41.7%; Score 466; DB 1; Length 108;
Best Local Similarity 82.4%; Pred. No. 4.7e-32;
Matches 89; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVTITCRASQDINNNYLNWYQOKPGKAPKLLIYVSTLHSGVPS 60
Db 1 DIQMTQSPSSLSASVGRVTITCRASQDINNNYLNWYQOKPGKAPKLLIYVSTLHSGVPS 60

Qy 61 RFSGSGSGDYTLTITSSLOPEDFATYCCQGNLPTPTFGGKTVEIKR 108
Db 61 RFSGSGSGDYSLTISLNLEQEDIATYFCQGGKTLPTFTGGGKTLEIKR 108

RESULT 8
KV10_HUMAN
ID KV10_HUMAN STANDARD; PRT; 108 AA.
AC P01607;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Rei.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=76023758; PubMed=809329;
RA Palm W., Hilschmann N.;
RT "The primary structure of a crystalline monoclonal immunoglobulin
RT kappa-type L-chain, subgroup I (Bence-Jones protein Rei); isolation
RT and characterization of the tryptic peptides; the complete amino acid
RT sequence of the protein; a contribution to the elucidation of the
RT three-dimensional structure of antibodies, in particular their
RT combining site.";
RL Hoppe-Seyler's Z. Physiol. Chem. 356:167-191(1975).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX MEDLINE=76039968; PubMed=1182131;
RA Epp O., Lattman E.E., Schiffer M., Huber R., Palm W.;
RT "The molecular structure of a dimer composed of the variable portions
RT of the Bence-Jones protein Rei refined at 2.0-A resolution.";
RL Biochemistry 14:4943-4952(1975).
CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
CC MARKER.
CC -!- MISCELLANEOUS: THIS IS A BENICE-JONES PROTEIN.

```

PIR; A01873; KIHURE.
DR PDB; 1REI; 17-FEB-84.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 107 FRAMEWORK-4.
FT DISULFID 23 88
FT STRAND 4 7
FT STRAND 10 13
FT TURN 15 16
FT STRAND 19 25
FT TURN 30 31
FT STRAND 33 38
FT TURN 40 41
FT STRAND 45 49
FT TURN 50 52
FT STRAND 53 54
FT TURN 56 57
FT TURN 60 61
FT STRAND 62 67
FT TURN 68 69
FT STRAND 70 75
FT HELIX 80 82
FT STRAND 85 90
FT STRAND 98 98
FT STRAND 102 106
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11902 MW; 9E8143E118BCE2A CRC64;

Query Match 41.5%; Score 464; DB 1; Length 108;
Best Local Similarity 83.3%; Pred. No. 6.8e-32;
Matches 90; Conservative 5; Mismatches 13; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVITCRASODINNYLNWYQKPKAPKLLIYYTSTLHSGVPS 60
|||||
DB 1 DIQMTQSPSSLSASVGRVITCRASODIINLYLNWYQQTGKAPKLLIYEASNLQAGVPS 60
|||||
QY 61 RFGSGSGTDYTLTISSLPQEDFATYYCQOGNTLPPTFGQGTKEIKR 108
|||||
DB 61 RFGSGSGTDYTLTISSLPQEDATYYCQYQSLPYTFGQGTKEIKR 108
|||||

RESULT 9
KVIA_HUMAN STANDARD; PRT; 108 AA.
AC P01593;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region AG.
OS Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=69234734; PubMed=4893682;
RA Titani K., Shinoda T., Putnam F.W.;
RT "The amino acid sequence of a kappa type Bence-Jones protein. 3. The
complete sequence and the location of the disulfide bridges.";
J. Biol. Chem. 244:3550-3560(1969).
CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR PIR; A01861; KIHUAG.

HSP: P01607; 1REI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 107 FRAMEWORK-4.
FT DISULFID 23 88
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11992 MW; E3B3B246C18F0C4F CRC64;

Query Match 41.4%; Score 463; DB 1; Length 108;
Best Local Similarity 82.4%; Pred. No. 8.2e-32;
Matches 89; Conservative 7; Mismatches 12; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVITCRASODINNYLNWYQKPKAPKLLIYYTSTLHSGVPS 60
|||||
DB 1 DIQMTQSPSSLSASVGRVITCRASODINHYLNWYQKPKAPKLLIYDASNLETGVPS 60
|||||
QY 61 RFGSGSGTDYTLTISSLPQEDFATYYCQOGNTLPPTFGQGTKEIKR 108
|||||
DB 61 RFGSGSGTDYTLTISSLPQEDATYYCQYQDTLPRTFGQGTKEIKR 108
|||||

RESULT 10
KV5K_MOUSE STANDARD; PRT; 108 AA.
AC P01644;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-V region HP R16.7.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.

RC STRAIN-A/J;
RX MEDLINE=82150934; PubMed=6801658;
RA Siegelman M., Capra J.D.;
RT "Complete amino acid sequence of light chain variable regions derived
from five monoclonal anti-p-azophenylarsonate antibodies differing
with respect to a crossreactive idiotype.";
Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).
CC -!- MISCELLANEOUS: ANTI-ARSONATE HYBRIDOMA PROTEIN.
DR PIR; A01927; KVMASR.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Antiarsenate antibody.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 108 FRAMEWORK-4.
FT NON_TER 108 108 BY SIMILARITY.
SQ SEQUENCE 108 AA; 11910 MW; A554642C63EFF597 CRC64;

Query Match 41.4%; Score 463; DB 1; Length 108;
Best Local Similarity 81.5%; Pred. No. 8.2e-32;

```
Matches 88; Conservative 10; Mismatches 10; Indels 10; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVITTCRASQDINNLYNWYQKPGKAPKLLIYYTSTLHSGVPS 60
DB 1 DIQMTQSSLSASLGRVITTCRASQDINNLYNWYQKPGDGTVKLLIYYTSLHSGVPS 60
QY 61 RFSGSGSGTDYTLTISSLPEDFATYYCQGNLTLPPTFGQGTKEIKR 108
DB 61 RFSGSGSGTDYSLTISNLEQEDATYFCQGNLSLPTFGGKLEIKR 108

RESULT 11
KV5L_MOUSE
ID KV5L_MOUSE STANDARD; PRT; 108 AA.
AC P01645;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-V region HP 93G7.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RC STRAIN=A/J;
RX MEDLINE=821150934; PubMed=6801658;
RA Siegelman M., Capra J.D.;
RT "Complete amino acid sequence of light chain variable regions derived
RT from five monoclonal anti-p-azophenylarsenate antibodies differing
RT with respect to a crossreactive idiotype.";
RL Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).
CC -!- MISCELLANEOUS: ANTI-ARSONATE HYBRIDOMA PROTEIN.
DR PIR: A01927; KVMRSAR.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
KW Immunoglobulin V region; Antiarsonate antibody.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 108 FRAMEWORK-4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11954 MW; 22F4642C63EFF58E CRC64;

Query Match 41.2%; Score 461; DB 1; Length 108;
Best Local Similarity 81.5%; Pred. No. 1.2e-31;
Matches 88; Conservative 9; Mismatches 11; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVITTCRASQDINNLYNWYQKPGKAPKLLIYYTSTLHSGVPS 60
DB 1 DIQMTQSSLSASLGRVITTCRASQDINNLYNWYQKPGDGTVKLLIYYTSLHSGVPS 60
QY 61 RFSGSGSGTDYTLTISSLPEDFATYYCQGNLTLPPTFGQGTKEIKR 108
DB 61 RFSGSGSGTDYSLTISNLEQEDATYFCQGNLSLPTFGGKLEIKR 108

RESULT 12
KVIV_HUMAN
ID KVIV_HUMAN STANDARD; PRT; 108 AA.
AC P04430;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region BAN.
OS Homo sapiens (Human).
```

```
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=86174817; PubMed=3083240;
RA Dwulet F.E., O'Connor T.P., Benson M.D.;
RT "Polymorphism in a kappa I primary (AL) amyloid protein (BAN).";
RL Mol. Immunol. 23:73-78(1986).
DR PIR: A01878; K1HUBN.
DR HSSP: P80362; 1WTL.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
KW Immunoglobulin V region; Amyloid.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 107 FRAMEWORK-4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11840 MW; CD3FD944FE96FD37 CRC64;

Query Match 41.1%; Score 459; DB 1; Length 108;
Best Local Similarity 81.5%; Pred. No. 1.8e-31;
Matches 88; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVITTCRASQDINNLYNWYQKPGKAPKLLIYYTSTLHSGVPS 60
DB 1 DIQMTQSSLSASVGRVITTCRASQSYNYVAVFQKPGKAPKLLIYDASTLQSGVPS 60
QY 61 RFSGSGSGTDYTLTISSLPEDFATYYCQGNLTLPPTFGQGTKEIKR 108
DB 61 NFGTSGSGTDFLTITISLQPEDFATYYCQYNSPYTFGGQTKVQIKR 108

RESULT 13
KVIV_HUMAN
ID KVIV_HUMAN STANDARD; PRT; 129 AA.
AC P04431;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Walker precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85014148; PubMed=6091049;
RA Klobbeck H.G., Combratio G., Zachau H.G.;
RT "Immunoglobulin genes of the kappa light chain type from two human
RT lymphoid cell lines are closely related.";
RL Nucleic Acids Res. 12:6995-7006(1984).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: X00965; CAA25477.1; ALT_TERM.
DR PIR: A01883; K1HUKK.
DR HSSP: P01607; 1REI.
DR InterPro: IPR003006; Ig_MHC.
```

DR	InterPro:	IPR003596;	Ig_v.
DR	Pfam:	PF00047;	Ig; 1.
DR	SMART:	SM00406;	IGV; 1.
KW	Immunoglobulin v region;	Signal.	
FT	SIGNAL	1	22
FT	CHAIN	23	129
FT	DOMAIN	23	45
FT	DOMAIN	46	56
FT	DOMAIN	57	71
FT	DOMAIN	72	78
FT	DOMAIN	79	110
FT	DOMAIN	111	119
FT	DOMAIN	120	129
FT	DISULFID	45	110
FT	NON_TER	129	129
SEQ	SEQUENCE	129 AA;	14069 MW; F941FA07D4AFC3F9 CRC64;

Query Match	41.1%;	Score 459;	DB 1;	Length 129;
Best Local Similarity	84.1%;	Pred. No. 2.2e-31;		
Matches	90;	Conservative	6;	Mismatches 11; Indels 0; Gaps 0;

QY	1	DIQMTQSPSSLSASVGDRVTITCRASDIINLYNWYQQKPKGAPKLLIYYTSTLHSGVPS	60
Db	23	DIQMTQSPSSLSASVGDRVTITCRASISINLYNWYQQKPKGAPKLLIIAAASSIQSGVTS	82
QY	61	RFGSGSGTDYTLRISSLPEDFATYYCQCQNTLPPTFGQGTKVEIK	107
Db	83	RFGSGSGTDFTLISSLPEDSATYYCQSYSLTITFGQGRLEIK	129


```

RESULT 14
KVIE_HUMAN STANDARD; PRT; 108 AA.
AC P01597;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region DEE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RS SEQUENCE.
RX MEDLINE=72053133; PubMed=5124396;
RA Milstein C.P.; Deverson E.V.;
RT "The amino acid sequence of a human kappa light chain.";
RL Biochem. J. 123:943-958(1971).
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
DR HSSP; P01607; IREI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin v region.
FT DOMAIN 1 23
FT FT 24 34
FT DOMAIN 35 49
FT DOMAIN 50 56
FT DOMAIN 57 88
FT DOMAIN 89 97
FT DOMAIN 98 107
FT DISULFID 23 88
FT NON_TER 108 108
SEQ SEQUENCE 108 AA; 11661 MW; BDDGE350017FLF51 CRC64;

```


Query Match	40.8%;	Score 456;	DB 1;	Length 108;
Best Local Similarity	79.6%;	Pred. No. 3.1e-31;		
Matches	86;	Conservative	8;	Mismatches 14; Indels 0; Gaps 0;

Result No.	Score	§		Length	DB	ID	Description
		Query Match					
1	794	71.0	234	11	Q91WF8	Q91wf8	mus musculus
2	784	70.1	233	11	Q91WS9	Q91ws9	mus musculus
3	742	66.4	214	11	Q91IA5	Q91ia5	mus musculus
4	701.5	62.7	238	11	Q99W37	Q99w37	mus musculus
5	701	62.7	211	11	Q91XL0	Q91xl0	mus musculus
6	689.5	61.7	235	11	Q91WL2	Q91wl2	mus musculus
7	474	42.4	108	4	Q9UL77	Q9ul77	homo sapien
8	470.5	42.1	107	4	Q96SA9	Q96sa9	homo sapien
9	467	41.8	108	4	Q9UL70	Q9ul70	homo sapien
10	466	41.7	116	4	Q96PF6	Q96pf6	homo sapien
11	451	40.3	108	4	Q9UL79	Q9ul79	homo sapien
12	449.5	40.2	107	4	Q9UL81	Q9ul81	homo sapien
13	410	36.7	298	11	Q9QZF0	Q9qzf0	mus musculus
14	404.5	36.2	236	4	Q96E61	Q96e61	homo sapien
15	403	36.0	109	11	Q92OE6	Q92oe6	mus musculus
16	391	35.0	107	11	Q9JL84	Q9j184	mus musculus

DR	SMART; SM00406; IGV; 1.
DR	SMART; SM00410; IG_like; 1.
DR	PROSITE; PS00290; IG_MHC; UNKNOWN_1.
FT	NON_TER 1 214
FT	NON_TER 214 214
SQ	SEQUENCE 214 AA; 23922 MW; 52BA205FDE995E2A CRC64;

Query Match	66.4%; Score 742; DB 11; Length 214;
Best Local Similarity	65.0%; Pred. No. 1.5e-60;
Matches 139; Conservative	29; Mismatches 46; Indels 0; Gaps 0;

QY	1 DIQMWTQSPSSLSASVGRVTITCRASDINNLYNMYOQKPGAPKLIIYYTSTLHSGVPS 60
Db	1 DIQLTQSPSSMYASLGERTVITCKASDINSYLSWFOQKPKGSKPTLIYRANRLVDGVPS 60
QY	61 RFSGSGSDTYLTISSLPEDFATYYCOQGNTPPPFGQTKEIKRTVAAPSVFIEPP 120
Db	61 RFSGSGSQDYSLTISSEYDMGIYCLQYDEFPFFTGSGTKLEIKRADAAPTVSIFPP 120
QY	121 SDEOLKGSTASVCLLNPNPREAKVQKVNDNALQSGNSQSBSVTEQDSKDYTSYSSLT 180
Db	121 SSEOLTSGGASVCFLNPFYKDINVKWKIDGSRQNGVLNSWTDDQDSKDYTSMSSTLT 180
QY	181 LSKADYEKKHYACEVTHQGLSSPVTXFNREGC 214
Db	181 LTKDEYERHNSYTCEATHKTSTSPIVCFNRNEC 214

RESULT 4	
ID Q99M37	PRELIMINARY; PRT; 238 AA.
AC O99M37;	
DT 01-JUN-2001	(TrEMBLrel. 17, Created)
DT 01-JUN-2001	(TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001	(TrEMBLrel. 19, Last annotation update)
DE	HYPOTHETICAL 26.3 KDA PROTEIN.
OS Mus musculus (Mouse).	
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
OX NCBI_TaxId=10090;	
RN [1]	
RP SEQUENCE FROM N.A.	
RC TISSUE=MAMMARY TUMOR. WAP-TGF ALPHA MODEL. 7 MONTHS OLD, GROSS	
RC TISSUE;	
RA Strausberg R.;	
RL Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.	
DR EMBL; BC002035; AAH02035.1; -;	
DR HSSP; P01679; 2FBJ.	
DR InterPro; IPR003599; Ig.	
DR InterPro; IPR003597; Ig.cl.	
DR InterPro; IPR003600; Ig_like.	
DR InterPro; IPR003006; Ig_MHC.	
DR InterPro; IPR003596; Ig_v.	
DR Pfam; PF00047; Ig; 2.	
DR SMART; SM00409; IG; 2.	
DR SMART; SM00407; IGC1; 1.	
DR SMART; SM00406; IGV; 1.	
DR SMART; SM00410; IG_like; 1.	
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.	
DR Hypothetical protein.	
KW	
SQ SEQUENCE 238 AA; 26344 MW; FB2B06A0B801330A CRC64;	

Query Match	62.7%; Score 701.5; DB 11; Length 238;
Best Local Similarity	60.3%; Pred. No. 9.2e-57;
Matches 132; Conservative	30; Mismatches 52; Indels 5; Gaps 1;

QY	1 DIQMWTQSPSSLSASVGRVTITCRASDI-----NNYLNMWYQOKPGKAPKLIIYTTSLH 55
Db	20 DVMTQTPLSLVSLGDQAQSIICKRSQSVHSNGNTLTWLTLQPKGSKPLIITYKVSNR 79
QY	56 SGVPFRFSGSGSDTYLTITSSLPEDFAFYICQQGNTPPTFCQGKVEIKRTVAAPS 115

```

Db 80 SCVPRFSGSGTDTFTLKISRAVEADLGYYVYFQGSHPVYTFGSGPKLEIKRADAAPTY 139
QY 116 FTFPSDEQLKSGTASVWCLNNFYPREAKVQKVDNALQSGNSQSVTEQDSKDSYSTSL 175
Db 140 SIFPPSEQLTSGGASVGVFLNNFYPKDINVKWKIDGSRQNGVLNSWTDQDSKDSYSTSM 199
QY 176 SSTLTLSKADYEKKHKVYACEVTHOGLSSPVTKSFNRGEC 214
Db 200 SSTLTLDKDEYERHNSYTCEATHKSTSTSPIVKSFNREK 238

RESULT 5
Q91XL0 PRELIMINARY; PRT; 211 AA.
AC Q91XL0;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE ADULT MALE KIDNEY CDNA, RIKEN FULL-LENGTH ENRICHED LIBRARY,
DE CLONE:0610010P20, FULL INSERT SEQUENCE.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=KIDNEY;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Aono H., Arai A.,
RA Arakawa T., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA Imotani K., Ishii Y., Itoh M., Izawa M., Kato H., Kawai J., Kojima Y.,
RA Konno H., Kouda M., Koya S., Kurihara C., Matsuyama T., Miyazaki A.,
RA Nishi K., Nomura K., Nunazaki R., Ohno M., Okazaki Y., Okido T.,
RA Owa C., Saito H., Saito R., Sakai C., Sakai K., Sano H., Sasaki D.,
RA Shibata K., Shibata Y., Shinagawa A., Shiraki T., Sogabe Y.,
RA Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T., Tejima Y.,
RA Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=KIDNEY;
RX MEDLINE=21085660; PubMed=11217851;
RA RIKEN FANTOM Consortium.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=KIDNEY;
RX MEDLINE=99279253; PubMed=10349636;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=KIDNEY;
RX MEDLINE=20499374; PubMed=11042159;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=KIDNEY;
RX MEDLINE=20530913; PubMed=11076861;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,

```

```

RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
DR EMBL; AK002514; BAB22154.1; -.
SQ SEQUENCE 211 AA; 23182 MW; 1A5FFA0F8BA50163 CRC64;

Query Match 62.7%; Score 701; DB 11; Length 211;
Best Local Similarity 63.0%; Pred. No. 8.8e-57;
Matches 133; Conservative 29; Mismatches 49; Indels 0; Gaps 0;

QY 4 MTQSPSSLSASVGDRTVITCRASODINNNYQKPKAPKLLIYYTSLHSGVPSRF 63
Db 1 MTQSPASLSVSVGETVTITCRASENIYSLNLAQYQKQKSPOLLVYATNADGVPSRF 60

QY 64 GSGGTDYTLTSSLOPEDFATYYCOQGNLTLPPTFGQGTKEIKRTVAAPSVFIFPPSDE 123
Db 1 GSGGTDYTLTSSLOPEDFATYYCOQGNLTLPPTFGQGTKEIKRTVAAPSVFIFPPSDE 120

QY 124 QLKSGTASVWCLNNFYPREAKVQKVDNALQSGNSQSVTEQDSKDSYSTSLTSLK 183
Db 121 QLTSGGASVWCLNNFYPKDINVKWKIDGSRQNGVLNSWTDQDSKDSYSTSLTSLK 180

QY 184 ADYEKKHKVYACEVTHOGLSSPVTKSFNRGEC 214
Db 181 DEYERHNSYTCEATHKSTSTSPIVKSFNREK 211

RESULT 6
Q91WL2 PRELIMINARY; PRT; 235 AA.
AC Q91WL2;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE UNKNOWN (PROTEIN FOR MGC:6582).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BREAST TUMOR;
RA Strausberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC006643; AAH06643.1; -.
SQ SEQUENCE 235 AA; 26021 MW; 5FC73BDEBD5E8FEF CRC64;

Query Match 61.7%; Score 689.5; DB 11; Length 235;
Best Local Similarity 61.0%; Pred. No. 1.2e-55;
Matches 130; Conservative 33; Mismatches 49; Indels 1; Gaps 1;

QY 2 IQMTQSPSSLSASVGDRTVITCRASODINNNYQKPKAPKLLIYYTSLHSGVPSR 61
Db 24 IVLQSPASLSASVGETVTITCRASENIYSLNLAQYQKQKSPOLLVYATNADGVPSR 82

QY 62 FSGGSGTDYTLTSSLOPEDFATYYCOQGNLTLPPTFGQGTKEIKRTVAAPSVFIFPPS 121
Db 83 FSGGSGTSLTISNMEADVATYYCOQWSRNPPTFGVGTKEIKRADAAPTVSIFFPS 142

QY 122 DEQLKSGTASVWCLNNFYPREAKVQKVDNALQSGNSQSVTEQDSKDSYSTSLTSL 181
Db 143 SEQLTSGGASVWCLNNFYPKDINVKWKIDGSRQNGVLNSWTDQDSKDSYSTSLTSL 202

QY 182 SKADYEKKHKVYACEVTHOGLSSPVTKSFNRGEC 214
Db 203 TKDEYERHNSYTCEATHKSTSTSPIVKSFNREK 235

RESULT 7
Q9UL77

```

```

ID Q9UL77 PRELIMINARY; PRT; 108 AA.
AC Q9UL77;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION
DE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035037; AAD56273.1; -.
DR HSSP; P01607; IREI.
DR InterPro; IPR003006; Iq_MHC.
DR InterPro; IPR003596; Iq_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; Igv; 1.
DR NON_TER 1
FT NON_TER 108
SQ SEQUENCE 108 AA; 11738 MW; C06681716C4D16F3 CRC64;

Query Match 42.4%; Score 474; DB 4; Length 108;
Best Local Similarity 85.2%; Pred. No. 2.9e-36;
Matches 92; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITCRASODINNYLNWYQKPKAPKLLIYVSTLHSGVPS 60
Db 1 DIQMTQSPSSLSASVGDRTVITCRASODINNYLNWYQKPKAPKLLIYVSTLHSGVPS 60

QY 61 RFSGSGSGTDYTLTISLQPEDFATYCCQGNTPPTFGQGTKEIKR 108
Db 61 RFSGSGSGTDFTLTISLQPEDFATYCCQSYSTL--TFGGGTKEIKR 108

RESULT 8
Q96SA9 PRELIMINARY; PRT; 107 AA.
ID Q96SA9;
AC Q96SA9;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE ANTI-STREPTOCOCCAL/ANTI-MYOSIN IMMUNOGLOBULIN KAPPA LIGHT CHAIN
DE VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98375893; PubMed=9712075;
RA Aderson E.E., Shikhan A.R., Ward K.E., Cunningham M.W.;
RT "Molecular analysis of polyreactive monoclonal antibodies from
RT rheumatic carditis: human anti-N-acetylglucosamine/anti-myosin
RT antibody v region genes.";
RL J. Immunol. 161:2020-2031(1998).
DR EMBL; U96396; AAB68785.1; -.
DR NON_TER 1
FT NON_TER 107
SQ SEQUENCE 107 AA; 11520 MW; 4BB43E9C5B577F16 CRC64;

Query Match 42.1%; Score 470.5; DB 4; Length 107;
Best Local Similarity 87.2%; Pred. No. 6.1e-36;
Matches 95; Conservative 5; Mismatches 6; Indels 3; Gaps 2;

```

```

QY 1 DIQMTQSPSSLSASVGDRTVITCRASODINNYLNWYQKPKAPKLLIYVSTLHSGVPS 60
Db 1 DIQMTQSPSSLSASVGDRTVITCRASODINNYLNWYQKPKAPKLLIYVSTLHSGVPS 60

QY 61 RFSGSGSGTDYTLTISLQPEDFATYCCQGNTPPTFGQGTKEIKR 108
Db 61 RFSGSGSGTDFTLTISLQPEDFATYCCQSYSTL--TFGGGTKEIKR 107

RESULT 9
Q9UL70 PRELIMINARY; PRT; 108 AA.
ID Q9UL70;
AC Q9UL70;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION
DE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035044; AAD56280.1; -.
DR HSSP; P01607; IREI.
DR InterPro; IPR003006; Iq_MHC.
DR InterPro; IPR003596; Iq_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; Igv; 1.
DR NON_TER 1
FT NON_TER 108
SQ SEQUENCE 108 AA; 11633 MW; B7BEDC3E41FCCA37 CRC64;

Query Match 41.8%; Score 467; DB 4; Length 108;
Best Local Similarity 84.3%; Pred. No. 1.3e-35;
Matches 91; Conservative 5; Mismatches 12; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITCRASODINNYLNWYQKPKAPKLLIYVSTLHSGVPS 60
Db 1 DIQMTQSPSSLSASVGDRTVITCRASODINNYLNWYQKPKAPKLLIYVSTLHSGVPS 60

QY 61 RFSGSGSGTDYTLTISLQPEDFATYCCQGNTPPTFGQGTKEIKR 108
Db 61 RFSGSGSGTDFTLTISLQPEDFATYCCQKYNAPRTFGGTKEIKR 108

RESULT 10
Q96PF6 PRELIMINARY; PRT; 116 AA.
ID Q96PF6;
AC Q96PF6;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE KAPPA 1 LIGHT CHAIN VARIABLE REGION (FRAGMENT).
GN SDNK1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21361171; PubMed=11468171;
RA Comenzo R.L., Zhang Y., Martinez C., Osman K., Herrera G.A.;
RT "The tropism of organ involvement in primary systemic amyloidosis:

```


GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 14, 2002, 11:00:45 ; Search time 54.11 seconds
(without alignments)
439.286 Million cell updates/sec

Title: US-09-811-384-11

Perfect score: 1118

Sequence: 1 DIQMTQSPSSLSASVGRVT.....EVTHQGLSPVTKSFNRGEC 214

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

```
A_Geneseq_032802.*
1: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/AA1980.DAT.*
2: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/AA1981.DAT.*
3: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/AA1982.DAT.*
4: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/AA1983.DAT.*
5: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/AA1984.DAT.*
6: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/AA1985.DAT.*
7: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/AA1986.DAT.*
8: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/AA1987.DAT.*
9: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/AA1988.DAT.*
10: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/AA1989.DAT.*
11: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/AA1990.DAT.*
12: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/AA1991.DAT.*
13: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/AA1992.DAT.*
14: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/AA1993.DAT.*
15: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/AA1994.DAT.*
16: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/AA1995.DAT.*
17: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/AA1996.DAT.*
18: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/AA1997.DAT.*
19: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/AA1998.DAT.*
20: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/AA1999.DAT.*
21: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/AA2000.DAT.*
22: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT.*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1118	100.0	214	18 AAW34504	Light chain of hum
2	1118	100.0	214	18 AAW34506	Light chain of ful
3	1118	100.0	214	20 AAY08754	Human antibody huH
4	1118	100.0	214	20 AAW95615	Humanized anti-CD1
5	1118	100.0	214	20 AAW30632	Recombinant humani
6	1118	100.0	214	22 AAB66777	rhumaB CD18 light
7	1118	100.0	233	14 AAR30777	pH52-9.0 humanised
8	1118	100.0	237	20 AAW95622	psi130 expression
9	1118	100.0	237	20 AAW30634	Recombinant humani
10	1118	100.0	237	22 AAB66784	Protein encoded by
11	1118	100.0	537	21 AAB03664	Anti-CD18 antibody

12	1089	97.4	214	14 AAR43338	Completely humanis
13	1089	97.4	214	19 AAW49815	Amino acid sequenc
14	1069	95.6	367	21 AAY55078	Single chain Fv pr
15	1069	95.6	626	21 AAY55081	Single chain Fv pr
16	1068	95.5	237	19 AAW70703	Protein encoded by
17	1035	92.6	214	14 AAR30776	H52L6-158 murine a
18	1032.5	92.4	237	21 AAY96298	Human IGFAN-10 imm
19	1031	92.2	237	13 AAR24047	Light chain of 4D5
20	1031	92.2	513	22 AAB82924	Anti-HER2 Humab4D5
21	1031	92.2	698	20 AAW83493	4D5 Fab molecule e
22	1029	92.0	214	21 AAY93735	The kappa chain of
23	1028.5	92.0	237	21 AAY96289	Human IGFAN-1 immu
24	1026	91.8	240	22 AAG36665	Amino acid sequenc
25	1024	91.6	214	17 AAW00373	Anti-CD18 chimeric
26	1024	91.6	234	12 AAR13050	CD4-specific CDR-g
27	1021	91.3	218	18 AAW13563	Humanised anti-L-s
28	1018	91.1	236	21 AAY96297	Human IGFAN-9 immu
29	1016.5	90.9	237	21 AAY96301	Human IGFAN-13 imm
30	1016	90.9	218	20 AAW95658	Mus musculus anti-
31	1016	90.9	218	21 AAY85200	Light chain amino
32	1016	90.9	218	22 AAB76947	Full variable ligh
33	1015	90.8	234	18 AAW10233	TrF8-5G9 CDR-grafte
34	1014	90.7	233	13 AAR22754	Reshaped CAMPATH-1
35	1014	90.7	238	21 AAW90930	Humanised anti-Fas
36	1013	90.6	218	20 AAW95669	Mus musculus anti-
37	1013	90.6	218	20 AAW95664	Mus musculus anti-
38	1013	90.6	218	22 AAB47087	Anti-IgE antibody,
39	1013	90.6	218	22 AAB76949	Full length light
40	1013	90.6	218	22 AAB76951	Full length light
41	1013	90.6	218	22 AAB76953	Variable light cha
42	1013	90.6	218	22 AAB76958	Variable light cha
43	1013	90.6	238	21 AAW90932	Humanised anti-Fas
44	1011	90.4	214	20 AAY08600	JP11127855 Seq ID
45	1011	90.4	218	20 AAY50030	Human F27 anti-IgE

ALIGNMENTS

```
RESULT 1
AAW34504
ID AAW34504 standard; protein; 214 AA.
XX
XX AAW34504;
AC
DT
XX 19-MAR-1998 (first entry)
DE
XX Light chain of humanised H52 antibody.
XX
```

```
XX Humanised antibody: HuH52; light chain; focal ischaemic stroke; embolism;
KW brain damage; anti-CD18 antibody; cerebral blood flow; thromboembolism;
KW transient ischaemic attack; thrombolytic therapy; thrombosis; therapy;
KW systemic hypoperfusion; cardiac arrest.
XX
XX Synthetic.
OS Homo sapiens.
OS Mus sp.
XX
XX WO9726912-A2.
XX
XX 31-JUL-1997.
XX
```

```
XX 11-JAN-1997; 97WO-US00492.
XX
XX 23-JAN-1996; 96US-0589982.
XX
```

```
XX (GETH ) GENENTECH INC.
XX (UYVE-) UNIV VERMONT & STATE AGRIC COLLEGE.
XX
```

```
XX Bednar MM, Gross CE, Thomas GR;
XX
```

```
XX WPI; 1997-393373/36.
XX
```


PT Administering an anti-CD18 antibody to treat focal ischaemic stroke
PT - by increasing cerebral blood flow and reducing size of brain
PT infarct
XX
XX
PS Disclosure; Page 9; 4lpp; English.
XX
CC This sequence represents the light chain of the humanised H52 antibody.
CC The H52 antibody can be used in the method of the invention. The method
CC is for treating focal ischaemic stroke, i.e. damage to the brain due to
CC interrupted blood supply, in a mammal, caused by obstruction of a main
CC cerebral artery, comprises administering anti-CD18 antibody to increase
CC cerebral blood flow and/or reduce the size of the area of brain that
CC dies, without removing the arterial obstruction. CD18, is upregulated in
CC patients after ischaemic stroke or transient ischaemic attack (stroke
CC symptoms last less than 24 hours with complete recovery). Treatment with
CC anti-CD18 antibodies can increase cerebral blood flow and/or reduce brain
CC infarct size, improving clinical outcomes in focal ischaemic strokes in
CC mammals, particularly in humans. The method provides an alternative to
CC thrombolytic therapy for treating ischaemic strokes caused by
CC thromboembolism (thrombosis or embolism), particularly where thrombolytic
CC therapy has been unsuccessful, is contra-indicated e.g. because such
CC drugs exacerbate bleeding, or is unsuitable because of the time delay
CC between stroke onset and diagnosis. Thrombolytic agents (e.g. tissue
CC plasminogen activator) may also be administered before, after or
CC simultaneously with the anti-CD18 antibody. Alternatively, the method can
CC be used to treat the third main type of ischaemic stroke, systemic
CC hypoperfusion, e.g. resulting from cardiac arrest or drowning.
XX
SQ Sequence 214 AA;

Query Match 100.0%; Score 1118; DB 18; Length 214;
Best Local Similarity 100.0%; Pred. No. 2.4e-56;
Matches 214; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGDRTVITCRASQDINNLYNQKPGKAPKLLIYYTSTLHSGVPS 60
Db 1 diqmtqspsslsasvgdrtvitcrasqdinnlynwqkpgkapklliytstlshgvsps 60

Qy 61 RFSGSGSGTDYTLTISSLPQEDFATYYCOQGNTPPTFGQGTKEIKRTVAAPSVFIAPP 120
Db 61 rfsdgsdtdytlttisslqpedfatyccqgntlptfgggtkveikrtvaapsvfifpp 120

Qy 121 SDEQLKSGTASVYVCLLNFPYREKAVQWKVDNALQSGNSQESVTEQDSKSTYSLSSTLT 180
Db 121 sdeqlksgtasvcllnfnfypreakvqkvdnalgsgnsqesvteqdsksdystlsstlt 180

Qy 181 LSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 214
Db 181 lskadyekhkvacevthqglsspvtksfnrgec 214

RESULT 2
AAW34506
ID AAW34506 standard; protein; 214 AA.
XX
AC AAW34506;
XX
DT 19-MAR-1998 (first entry)
XX
DE Light chain of full length IgG2 humanised H52 antibody.
XX
KW Humanised antibody; Huh52; light chain; focal ischaemic stroke; embolism;
KW brain damage; anti-CD18 antibody; cerebral blood flow; thromboembolism;
KW transient ischaemic attack; thrombolytic therapy; thrombosis; therapy;
KW systemic hypoperfusion; cardiac arrest.
XX
OS Synthetic.
OS Homo sapiens.
OS Mus sp.
XX
PN W09726912-A2.
XX

PD 31-JUL-1997.
XX
PF 11-JAN-1997; 97WO-US00492.
XX
PR 23-JAN-1996; 96US-0589982.
XX
PA (GETH) GENENTECH INC.
PA (UYVE-) UNIV VERMONT & STATE AGRIC COLLEGE.
XX
PI Bednar MM, Gross CE, Thomas GR;
XX WPI; 1997-393373/36.
DR Administering an anti-CD18 antibody to treat focal ischaemic stroke
PT - by increasing cerebral blood flow and reducing size of brain
PT infarct
XX
PS Disclosure; Page 10; 4lpp; English.
XX
CC This sequence represents the light chain of the humanised H52 antibody.
CC The H52 antibody can be used in the method of the invention. The method
CC is for treating focal ischaemic stroke, i.e. damage to the brain due to
CC interrupted blood supply, in a mammal, caused by obstruction of a main
CC cerebral artery, comprises administering anti-CD18 antibody to increase
CC cerebral blood flow and/or reduce the size of the area of brain that
CC dies, without removing the arterial obstruction. CD18, is upregulated in
CC patients after ischaemic stroke or transient ischaemic attack (stroke
CC symptoms last less than 24 hours with complete recovery). Treatment with
CC anti-CD18 antibodies can increase cerebral blood flow and/or reduce brain
CC infarct size, improving clinical outcomes in focal ischaemic strokes in
CC mammals, particularly in humans. The method provides an alternative to
CC thrombolytic therapy for treating ischaemic strokes caused by
CC thromboembolism (thrombosis or embolism), particularly where thrombolytic
CC therapy has been unsuccessful, is contra-indicated e.g. because such
CC drugs exacerbate bleeding, or is unsuitable because of the time delay
CC between stroke onset and diagnosis. Thrombolytic agents (e.g. tissue
CC plasminogen activator) may also be administered before, after or
CC simultaneously with the anti-CD18 antibody. Alternatively, the method can
CC be used to treat the third main type of ischaemic stroke, systemic
CC hypoperfusion, e.g. resulting from cardiac arrest or drowning.
XX
SQ Sequence 214 AA;

Query Match 100.0%; Score 1118; DB 18; Length 214;
Best Local Similarity 100.0%; Pred. No. 2.4e-56;
Matches 214; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGDRTVITCRASQDINNLYNQKPGKAPKLLIYYTSTLHSGVPS 60
Db 1 diqmtqspsslsasvgdrtvitcrasqdinnlynwqkpgkapklliytstlshgvsps 60

Qy 61 RFSGSGSGTDYTLTISSLPQEDFATYYCOQGNTPPTFGQGTKEIKRTVAAPSVFIAPP 120
Db 61 rfsdgsdtdytlttisslqpedfatyccqgntlptfgggtkveikrtvaapsvfifpp 120

Qy 121 SDEQLKSGTASVYVCLLNFPYREKAVQWKVDNALQSGNSQESVTEQDSKSTYSLSSTLT 180
Db 121 sdeqlksgtasvcllnfnfypreakvqkvdnalgsgnsqesvteqdsksdystlsstlt 180

Qy 181 LSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 214
Db 181 lskadyekhkvacevthqglsspvtksfnrgec 214

RESULT 3
AAW08754
ID AAW08754 standard; protein; 214 AA.
XX
AC AAW08754;
XX
DT 10-AUG-1999 (first entry)
XX

DE Human antibody huH52 light chain protein fragment.
 XX IgG; immunoglobulin G; CH1 domain; human; anti-CD18; IgG1; IgG2; IgG3;
 KW IgG4; Kappa-CL domain; lambda-CL domain; focal ischaemic stroke;
 KW cerebroprotective; cerebral artery obstruction; blood flow; infarct;
 KW CD18 extracellular domain; endothelium; CD11b/CD18 complex dissociation;
 KW antibody; huH52; light chain.
 XX Homo sapiens.
 XX US5914112-A.
 XX 22-JUN-1999.
 XX 22-JAN-1997; 97US-0788800.
 XX 23-JAN-1996; 96US-0093038.
 XX 22-JAN-1997; 97US-0788800.
 XX (GETH) GENENTECH INC.
 XX (UYVE-) UNIV VERMONT & STATE AGRIC COLLEGE.
 XX Bednar MM, Gross CE, Thomas GR;
 XX WPI; 1999-370483/31.
 XX Anti-CD18 antibodies in stroke
 XX Claim 11; Column 31-32; 25pp; English.
 XX This invention describes a method for improving the clinical outcome in
 CC focal ischaemic stroke by administering novel anti-CD18 antibody which
 CC has cerebroprotective properties. The invention particularly describes a
 CC method of treating focal ischemic stroke caused by the obstruction of a
 CC main cerebral artery which comprises administering an anti-CD18 antibody
 CC to increase the blood flow or reduce the infarct size, where: (1) the
 CC antibody binds to an extracellular domain of CD18 and inhibits or reduces
 CC the ability of the cell expressing CD18 to bind to endothelium, (2) the
 CC antibody binds CD18 with an affinity of less than 4 nm, or (3) the
 CC antibody dissociates CD18/CD18 complex. This sequence represents the
 CC human antibody huH52 light chain region.
 XX
 SQ Sequence 214 AA;

Query Match 100.0%; Score 1118; DB 20; Length 214;
 Best Local Similarity 100.0%; Pred. No. 2.4e-56;
 Matches 214; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DIQMTQSPSSLSASVGRVTITCRASODINNYLNWYQKPGKAPKLLIYYTSTLHSGVPS 60
 Db 1 dIQMTQSPSSLSASVGRVTITCRASQDINNYLNWYQKPGKAPKLLIYYTSTLHSGVPS 60
 QY 61 RFSGSGGTDTYTLTISSLPQEDFATYYCQGGNTLPPTFGQGTKEIKRTVAAPSVEIFPP 120
 Db 61 rfsgsgsgtdytltlisslpqedfatyyccgqgntlpptfggktkeikrtvaapsvfifpp 120
 QY 121 SDEQLKSGTASVVCLLNFPYPRKAVQKVDNALQSGNSQESVTEQDSKDSYLSSTLT 180
 Db 121 sdeqlksgtasvvcllnfpypreakvqkvdnalqsgnsqesvteqdsksdystlsstlt 180
 QY 181 LSKADYEKKHYACEVTHQGLSSPVTKSFNRGEC 214
 Db 181 lskadyekhyacevthqglsspvtksfnrgec 214

RESULT 4
 AAW95615
 ID AAW95615 standard; protein; 214 AA.
 XX
 AC AAW95615;
 XX
 DT 08-JUN-1999 (first entry)

XX Humanized anti-CD18 antibody rhuMAB CD18 light chain.
 DE
 XX Monoclonal antibody; heavy chain; humanized; myocardial infarction;
 KW burns; thermal injury; ischemic; shock; ischaemic; haemorrhagic;
 KW hemorrhagic; stroke.
 XX Mus musculus.
 OS Synthetic.
 XX WO9856418-A1.
 XX 17-DEC-1998.
 XX 12-JUN-1998; 98WO-US12209.
 XX 13-JUN-1997; 97US-0874897.
 XX (GETH) GENENTECH INC.
 XX Lam XM, Oeswein JQ, Ongpipattanakul B, Shahrokh Z;
 PI Wang SX, Weissburg RP, Wong RL;
 XX WPI; 1999-080860/07.
 XX New stable aqueous antibody formulations - comprising an antibody
 PT not subjected to lyophilisation, a buffer maintaining the pH at 4.5
 PT - 6, a surfactant and a polyol
 XX Disclosure; Fig 1B; 87pp; English.
 PS
 XX The sequence is that of the heavy chain of a humanized murine
 CC anti-CD18 antibody rhuMAB CD18. It can be used for the treatment
 CC of disorders which include haemorrhagic shock, thermal injury (such
 CC as that resulting from burns), stroke (including ischaemic and
 CC haemorrhagic stroke) and myocardial infarction. The antibody
 CC formulation can be stabilised at a temperature of 2-8 deg. C
 CC for at least one year or at a temperature of 30 deg. C for at
 CC least one month and is stable following freezing and thawing.
 XX
 SQ Sequence 214 AA;

Query Match 100.0%; Score 1118; DB 20; Length 214;
 Best Local Similarity 100.0%; Pred. No. 2.4e-56;
 Matches 214; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DIQMTQSPSSLSASVGRVTITCRASODINNYLNWYQKPGKAPKLLIYYTSTLHSGVPS 60
 Db 1 dIQMTQSPSSLSASVGRVTITCRASQDINNYLNWYQKPGKAPKLLIYYTSTLHSGVPS 60
 QY 61 RFSGSGGTDTYTLTISSLPQEDFATYYCQGGNTLPPTFGQGTKEIKRTVAAPSVEIFPP 120
 Db 61 rfsgsgsgtdytltlisslpqedfatyyccgqgntlpptfggktkeikrtvaapsvfifpp 120
 QY 121 SDEQLKSGTASVVCLLNFPYPRKAVQKVDNALQSGNSQESVTEQDSKDSYLSSTLT 180
 Db 121 sdeqlksgtasvvcllnfpypreakvqkvdnalqsgnsqesvteqdsksdystlsstlt 180
 QY 181 LSKADYEKKHYACEVTHQGLSSPVTKSFNRGEC 214
 Db 181 lskadyekhyacevthqglsspvtksfnrgec 214

RESULT 5
 AAW30632
 ID AAW30632 standard; protein; 214 AA.
 XX
 AC AAW30632;
 XX
 DT 06-APR-1999 (first entry)
 XX
 DE Recombinant humanised anti-CD18 antibody rhuMAB CD18 light chain.

XX Recombinant humanised anti-CD18 antibody; rhuMAB CD18; leucine zipper;
KW murine monoclonal antibody; muMAB H52; protein recovery; filtration;
KW chromatography.
XX
OS Mus sp.
OS Homo sapiens.
OS Synthetic.
XX
PN W09856808-A1.
XX
XX 17-DEC-1998.
PD
XX 12-JUN-1998; 98WO-US12334.
PF
XX 13-JUN-1997; 97US-0050951.
PR
XX (GETH) GENENTECH INC.
PA
XX Blank GS, Narindray DS, Zapata GA;
PI
XX WPI; 1999-060267/05.
DR
XX
XX New method for recovering polypeptides from cell cultures - by
PT treating with reagent and filtering to remove reagent
PT
XX
XX Example; Fig 1B; 43pp; English.
PS
XX
XX A method has been developed for recovering a polypeptide comprising: (a)
CC exposing a composition comprising a polypeptide to a reagent which binds
CC to or modifies the polypeptide, where the reagent is immobilized on a
CC solid phase; and (b) passing the composition through a filter bearing an
CC opposite charge to the reagent so as to remove leached reagent from the
CC composition. The present invention also describes a method for modifying
CC a precursor antibody comprising a leucine zipper by exposing the
CC precursor antibody to a protease immobilized on a solid support so that
CC the protease removes the zipper. The methods can be used to purify
CC proteins from cell cultures. They are especially useful for isolating
CC antibodies. The methods overcome the problem of reagent leakage into the
CC protein as is the case in prior art immobilized modification systems. By
CC using a opposite charge filter the reagent can be excluded from the
CC sample, preventing contamination. The present sequence represents the
CC recombinant humanised anti-CD18 antibody (rhuMAB CD18) light chain,
CC which is used in an example from the present invention.
XX
SQ Sequence 214 AA;

Query Match 100.0%; Score 1118; DB 20; Length 214;
Best Local Similarity 100.0%; Pred. No. 2.4e-56;
Matches 214; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 DIQMTQSPSSLSASVGDRTVITCRASQDINNYLNWYQKPGKAPKLLIYYTSTLHSGVPS 60
Db 1 diqmtqspsslsasvgdrtvitcrasqdinnynlwyyqkpgkapklliyystlshsgvps 60
Qy 61 RFSGSGSDTYLTITSSLOPEFATYYCQGNLTLPPTFGQGTVEIKRTVAAPSVFIAPP 120
Db 61 rfs gsgsgtdy l t i s s l o p e f a t y y c q g n l t p p t f g g t v e i k r t v a a p s v f i a p p 120
Qy 121 SDEQLKSGTASVVCLLNFFYPREAKVQWVDNALQSGNSQESVTEQDSKDSYLSLSTLT 180
Db 121 sdeqlksgtasvvc l l n n f y p r e a k v q w v d n a l q s g n s q e s v t e q d s k d s t y l s l s t l t 180
Qy 181 LSKADYKHKVYACEVTHOGLSSPVTKSFNRGEC 214
Db 181 l s k a d y e k h k v y a c e v t h o g l s s p v t k s f n r g e c 214

RESULT 6
AAB66777
ID AAB66777 standard; protein; 214 AA.
XX

AAB66777;
XX 10-APR-2001 (first entry)
XX rhuMAB CD18 light chain.
XX
XX Antibody; lyophilization; hemorrhagic shock; thermal injury;
KW myocardial infarction; inflammation.
XX
XX Homo sapiens.
XX
XX US6171586-B1.
PN
XX 09-JAN-2001.
PD
XX 12-JUN-1998; 98US-0097171.
PF
XX 13-JUN-1997; 97US-0053087.
PR
XX (GETH) GENENTECH INC.
PA
XX
XX Lam XM, Oeswein JO, Ongpipattanakul B, Shahrokh Z, Wang SX;
PI Weissburg RP, Wong RL;
PI
XX WPI; 2001-136863/14.
DR
XX
XX Stable aqueous pharmaceutical formulation for treating hemorrhagic
PT shock, thermal injury, stroke, and myocardial infarction, comprises an
PT antibody not subjected to prior lyophilization -
PT
XX Example 1; Fig 1; 56pp; English.
PS
XX The present invention relates to a stable aqueous pharmaceutical
CC formulation, comprising an antibody not subjected to prior
CC lyophilization, an acetate buffer of pH 4.8-5.5, a surfactant and
CC a polyol. The invention is useful for treating hemorrhagic shock,
CC thermal injury, e.g. resulting from burns, stroke including
CC ischemic and hemorrhagic stroke, myocardial infarction,
CC inflammatory disorders such as adult respiratory distress
CC syndrome (ARDS), hypovolemic shock, ulcerative colitis, rheumatoid
CC arthritis and B-cell lymphomas.
XX
SQ Sequence 214 AA;

Query Match 100.0%; Score 1118; DB 22; Length 214;
Best Local Similarity 100.0%; Pred. No. 2.4e-56;
Matches 214; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 DIQMTQSPSSLSASVGDRTVITCRASQDINNYLNWYQKPGKAPKLLIYYTSTLHSGVPS 60
Db 1 diqmtqspsslsasvgdrtvitcrasqdinnynlwyyqkpgkapklliyystlshsgvps 60
Qy 61 RFSGSGSDTYLTITSSLOPEFATYYCQGNLTLPPTFGQGTVEIKRTVAAPSVFIAPP 120
Db 61 rfs gsgsgtdy l t i s s l o p e f a t y y c q g n l t p p t f g g t v e i k r t v a a p s v f i a p p 120
Qy 121 SDEQLKSGTASVVCLLNFFYPREAKVQWVDNALQSGNSQESVTEQDSKDSYLSLSTLT 180
Db 121 sdeqlksgtasvvc l l n n f y p r e a k v q w v d n a l q s g n s q e s v t e q d s k d s t y l s l s t l t 180
Qy 181 LSKADYKHKVYACEVTHOGLSSPVTKSFNRGEC 214
Db 181 l s k a d y e k h k v y a c e v t h o g l s s p v t k s f n r g e c 214

RESULT 7
AAR30777
ID AAR30777 standard; protein; 233 AA.
XX
XX AAR30777;
XX
XX 12-MAY-1993 (first entry)
DT

XX pH52-9.0 humanised murine anti-CD18 antibody light chain.
 DE Humanisation; rapid; monoclonal antibody.
 XX Mus musculus.
 KW WO9222653-A.
 XX 23-DEC-1992.
 PN 15-JUN-1992; 92WO-US05126.
 XX 14-JUN-1991; 91US-0715272.
 XX (GETH) GENENTECH INC.
 PA Carter PJ, Presta LG;
 PI WPI; 1993-018139/02.
 XX

XX Humanisation of antibodies - by molecular modelling of the variable
 PT domains and alteration by gene conversion mutagenesis
 XX
 XX Disclosure; Fig 6B; 126pp; English.
 PS The sequence is that of the humanised light chain sequence of
 CC murine anti-CD18 antibody pH52-9.0.
 XX
 XX Sequence 233 AA;

Query Match 100.0%; Score 1118; DB 14; Length 233;
 Best Local Similarity 100.0%; Pred. No. 2.6e-56;
 Matches 214; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DIQMTQSPSSLSASVGRVTITCRASQDINNYLNWYQKPGKAPKLLIYTTSTLHSGVPS 60
 DB 20 DIQMCPSPSSLSASVGRVTITCRASQDINNYLNWYQKPGKAPKLLIYTTSTLHSGVPS 79
 QY 61 RFGSGSGTDYTLTISSIQPEDFATYYCOQGNTLPTFGQGTKEIKRTVAAPSVFIAPP 120
 DB 80 RFGSGSGTDYTLTISSIQPEDFATYYCOQGNTLPTFGQGTKEIKRTVAAPSVFIAPP 139
 QY 121 SDEQLKSGTASVCLLNFPYREKAVQWKNALQSGNSQESVTEQDSKDSYLSSTLT 180
 DB 140 SDEQLKSGTASVCLLNFPYREKAVQWKNALQSGNSQESVTEQDSKDSYLSSTLT 199
 QY 181 LSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC 214
 DB 200 LSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC 233

RESULT 8
 AAW95622
 ID AAW95622 standard; Protein; 237 AA.
 XX
 AC AAW95622;
 XX
 DT 08-JUN-1999 (first entry)
 XX
 DE pS1130 expression cassette encoded rhuMab CD18 light chain.
 XX
 KW Monoclonal antibody; heavy chain; humanized; myocardial infarction;
 KW burns; thermal injury; ischemic; shock; ischemic; haemorrhagic;
 KW hemorrhagic; stroke; light chain.
 XX
 OS Mus musculus.
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FH Sig_peptide 1..23
 XX

PN WO9856418-A1.
 XX
 PD 17-DEC-1998.
 XX
 PF 12-JUN-1998; 98WO-US12209.
 XX
 PR 13-JUN-1997; 97US-0874897.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Lam XM, Oeswein JQ, Ongpipattanakul B, Shahrokh Z;
 PI Wang SX, Weissburg RP, Wong RL;
 XX
 DR WPI; 1999-080860/07.
 XX

XX New stable aqueous antibody formulations - comprising an antibody
 PT not subjected to lyophilisation, a buffer maintaining the pH at 4.5
 PT - 6, a surfactant and a polyol
 XX
 XX Disclosure; Fig 21A; 87pp; English.
 PS
 XX The sequence is that of the pS1130 encoded light chain of a humanized
 CC murine anti-CD18 antibody rhuMab CD18. It can be used for the treatment
 CC of disorders which include haemorrhagic shock, thermal injury (such
 CC as that resulting from burns), stroke (including ischaemic and
 CC haemorrhagic stroke) and myocardial infarction. The antibody
 CC formulation can be stabilised at a temperature of 2-8 deg. C
 CC for at least one year or at a temperature of 30 deg. C for at
 CC least one month and is stable following freezing and thawing.
 XX
 XX Sequence 237 AA;

Query Match 100.0%; Score 1118; DB 20; Length 237;
 Best Local Similarity 100.0%; Pred. No. 2.6e-56;
 Matches 214; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DIQMTQSPSSLSASVGRVTITCRASQDINNYLNWYQKPGKAPKLLIYTTSTLHSGVPS 60
 DB 24 DIQMCPSPSSLSASVGRVTITCRASQDINNYLNWYQKPGKAPKLLIYTTSTLHSGVPS 83
 QY 61 RFGSGSGTDYTLTISSIQPEDFATYYCOQGNTLPTFGQGTKEIKRTVAAPSVFIAPP 120
 DB 84 RFGSGSGTDYTLTISSIQPEDFATYYCOQGNTLPTFGQGTKEIKRTVAAPSVFIAPP 143
 QY 121 SDEQLKSGTASVCLLNFPYREKAVQWKNALQSGNSQESVTEQDSKDSYLSSTLT 180
 DB 144 SDEQLKSGTASVCLLNFPYREKAVQWKNALQSGNSQESVTEQDSKDSYLSSTLT 203
 QY 181 LSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC 214
 DB 204 LSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC 237

RESULT 9
 AAW30634
 ID AAW30634 standard; protein; 237 AA.
 XX
 AC AAW30634;
 XX
 DT 06-APR-1999 (first entry)
 XX
 DE Recombinant humanised anti-CD18 antibody rhuMab CD18 light chain.
 XX
 KW Recombinant humanised anti-CD18 antibody; rhuMab CD18; leucine zipper;
 KW murine monoclonal antibody; muMab H52; protein recovery; filtration;
 KW chromatography.
 XX
 OS Mus sp.
 OS Homo sapiens.
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FH

```
FT Peptide 1..23
FT /label= signal
XX WO9856808-A1.
XX 17-DEC-1998.
XX 12-JUN-1998; 98WO-US12334.
XX 13-JUN-1997; 97US-0050951.
XX (GETH ) GENENTECH INC.
XX Blank GS, Narindray DS, Zapata GA;
XX WPI; 1999-060267/05.
XX N-PSDB; AAX03840.
XX New method for recovering polypeptides from cell cultures - by
XX treating with reagent and filtering to remove reagent
XX Example; Fig 4; 43pp; English.
XX A method has been developed for recovering a polypeptide comprising: (a)
XX exposing a composition comprising a polypeptide to a reagent which binds
XX to or modifies the polypeptide, where the reagent is immobilized on a
XX solid phase; and (b) passing the composition through a filter bearing an
XX opposite charge to the reagent so as to remove leached reagent from the
XX composition. The present invention also describes a method for modifying
XX a precursor antibody comprising a leucine zipper by exposing the
XX precursor antibody to a protease immobilized on a solid support so that
XX the protease removes the zipper. The methods can be used to purify
XX proteins from cell cultures. They are especially useful for isolating
XX antibodies. The methods overcome the problem of reagent leakage into the
XX protein as is the case in prior art immobilized modification systems. By
XX using a opposite charge filter the reagent can be excluded from the
XX sample, preventing contamination. The present sequence represents the
XX recombinant humanised anti-CD18 antibody (rhuMAB CD18) light chain,
XX which is used in an example from the present invention.
XX Sequence 237 AA;

Query Match 100.0%; Score 1118; DB 20; Length 237;
Best Local Similarity 100.0%; Pred. No. 2.6e-56;
Matches 214; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRVTITCRASQDINNYLNWYQOKPGKAPKLLIYYTSTLHSGVPS 60
DB 24 diqmtqspsslsasvgdrvtitcrasqdinnylnwyqkpgkapklliytytstlhsgvps 83
QY 61 RFSGSGGTDYTLTISSLPQEDFATYYCQOGNTLPPTFGQGTKEIKRTVAAPSVEIFPP 120
DB 84 rfsqsgsgtdytltlisslpqedfatyyccqognlppptfgggtkveikrtvvaapsvfi 143
QY 121 SDEQLKSGTASVCLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYSTLSSTLT 180
DB 144 sdeqlksgtasvclnnfyprcakvqkvdnalqsgnsqesvteqdsksdyslstlt 203
QY 181 LSKADYEKKHYACEVTHQGLSSPVTKSFNRGEC 214
DB 204 lskadyekhkyacevthqglsspvtksfnrgec 237

RESULT 10
AAB66784
ID AAB66784 standard; protein; 237 AA.
XX
AC AAB66784;
XX
DT 10-APR-2001 (first entry)
XX
DE Protein encoded by ps 1130 expression cassette.
```

```
XX Antibody; lyophilization; hemorrhagic shock; thermal injury;
KW myocardial infarction; inflammation.
XX Homo sapiens.
XX US6171586-B1.
XX 09-JAN-2001.
XX 12-JUN-1998; 98US-0097171.
XX 13-JUN-1997; 97US-0053087.
XX (GETH ) GENENTECH INC.
XX Lam XM, Oeswein JQ, Ongpipattanakul B, Shahrokh Z, Wang SX;
PI Weissburg RP, Wong RL;
XX WPI; 2001-136863/14.
XX Stable aqueous pharmaceutical formulation for treating hemorrhagic
PT shock, thermal injury, stroke, and myocardial infarction, comprises an
PT antibody not subjected to prior lyophilization
XX Disclosure; Fig 21; 56pp; English.
XX The present invention relates to a stable aqueous pharmaceutical
CC formulation, comprising an antibody not subjected to prior
CC lyophilization, an acetate buffer of pH 4.8-5.5, a surfactant and
CC a polyol. The invention is useful for treating hemorrhagic shock,
CC thermal injury, e.g. resulting from burns, stroke including
CC ischemic and hemorrhagic stroke, myocardial infarction,
CC inflammatory disorders such as adult respiratory distress
CC syndrome (ARDS), hypovolemic shock, ulcerative colitis, rheumatoid
CC arthritis and B-cell lymphomas.
XX Sequence 237 AA;

Query Match 100.0%; Score 1118; DB 22; Length 237;
Best Local Similarity 100.0%; Pred. No. 2.6e-56;
Matches 214; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRVTITCRASQDINNYLNWYQOKPGKAPKLLIYYTSTLHSGVPS 60
DB 24 diqmtqspsslsasvgdrvtitcrasqdinnylnwyqkpgkapklliytytstlhsgvps 83
QY 61 RFSGSGGTDYTLTISSLPQEDFATYYCQOGNTLPPTFGQGTKEIKRTVAAPSVEIFPP 120
DB 84 rfsqsgsgtdytltlisslpqedfatyyccqognlppptfgggtkveikrtvvaapsvfi 143
QY 121 SDEQLKSGTASVCLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYSTLSSTLT 180
DB 144 sdeqlksgtasvclnnfyprcakvqkvdnalqsgnsqesvteqdsksdyslstlt 203
QY 181 LSKADYEKKHYACEVTHQGLSSPVTKSFNRGEC 214
DB 204 lskadyekhkyacevthqglsspvtksfnrgec 237

RESULT 11
AAB03664
ID AAB03664 standard; Protein; 537 AA.
XX
AC AAB03664;
XX
DT 04-OCT-2000 (first entry)
XX
DE Anti-CD18 antibody (rhuMAB CD18) light and heavy chain protein sequence.
XX Expression cassette; pSL130; rhuMAB CD18; monoclonal antibody;
KW biochemical lysis; polypeptide recovery; anti-CD18 antibody.
```

```
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT Region 1..248
XX FT /note= "Anti-CD18 light chain"
XX FT 249..537
XX FT /note= "Anti-CD18 heavy chain"
XX PN WO200024873-A1.
XX XX
XX PD 04-MAY-2000.
XX XX
XX PF 21-OCT-1999; 99WO-US24696.
XX XX
XX PF 28-OCT-1998; 98US-0106052.
XX XX
XX PA (GETH ) GENENTECH INC.
XX PI Leung WS, Swartz JR;
XX XX
XX DR WPI; 2000-350719/30.
XX DR N-PSDB; AAA53339, AAA53389.
XX XX
XX PT Process for large scale production and recovery of polypeptides from
XX PT bacterial cells using a method of biochemical lysis -
XX XX
XX PS Example 1; Fig 4; 64pp; English.
XX XX
XX CC This sequence represents the anti-CD18 antibody (rhumab CD18) light and
XX CC heavy chain amino acid sequences. Rhumab CD18 is a recombinant F(ab')2
XX CC antibody, which binds to the MAC-1 (CD11b/CD18) receptor, blocking
XX CC binding of neutrophils to the endothelium. The expression cassette is
XX CC used in an example of the process of the invention, for recovering a
XX CC heterologous polypeptide from bacterial cells using biochemical lysis.
XX CC The process is used for the large scale production and recovery of
XX CC polypeptides e.g. human insulin-like growth factor (IGF), DNase, vascular
XX CC endothelial growth factor (VEGF), anti-CD18 antibody or anti-CD18
XX CC antibody fragment from bacterial cells.
XX XX
XX SQ Sequence 537 AA;

Query Match 100.0%; Score 1118; DB 21; Length 537;
Best Local Similarity 100.0%; Pred. No. 5.4e-56;
Matches 214; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITCRASQDINNYLNWYQKPGKAPKLLIYTTSTLHSGVPS 60
DB 24 diqmtqspsslsasvgdrtvtitcrasqdinnynwyqkpgkapklllytstllhs9vps 83
QY 61 RFGSGSGTDYTLTISSLPQEDFATYYCQGGNTLPPTFGQGTKEIKRTVAAPSFIAPP 120
DB 84 rfsgsgsgtdytlttisslpqedfatyycggntlpptfgggtkveikrtvaapsvfifpp 143
QY 121 SDEQLKSGTASVCLLNFFYPREAKVQWKNALQSGNSQESVTQDSKDSYSLSTLT 180
DB 144 sdeqlksgtasvcllnffypreakvqwkvdnalqsgnsqesvteqgskdstyslsstlt 203
QY 181 LSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 214
DB 204 lskadyekhkvyacevthqglsspsvtksfnrgec 237

RESULT 12
AAR43338
ID AAR43338 standard; Protein; 214 AA.
XX
XX AAR43338;
XX AC
XX DT 29-NOV-1993 (first entry)
XX DE Completely humanised C4G1 Ig light chain.
```

```
XX Immunoglobulin; H-chain; platelet membrane glycoprotein; GP1IIa/IIb;
KW monoclonal antibody; platelet agglutination; humanised antibody.
XX OS Synthetic.
XX PN WO9313133-A.
XX PD 08-JUL-1993.
XX XX
XX PF 15-DEC-1992; 92WO-JP01630.
XX XX
XX PR 20-DEC-1991; 91US-0812111.
XX PR 09-JUN-1992; 92US-0895952.
XX PR 11-SEP-1992; 92US-0944159.
XX XX
XX PA (PROT-) PROTEIN DESIGN LABS INC.
XX PA (YAMA ) YAMANOUCHI PHARM CO LTD.
XX PI Co MS, TSO JY;
XX XX
XX DR WPI; 1993-227275/28.
XX XX
XX PT Compsn. contg. immunoglobulin specific for the GP-1Ib and -IIIA
XX PT protein - for treating disorders related to vascular thrombosis
XX PS Claim 26; Fig 5C; 54pp; Japanese.
XX XX
XX CC This is the sequence of the humanised C4G1 immunoglobulin light
XX CC chain fragment. See AAR43339 for the heavy chain sequence. The
XX CC antibody is specific for the platelet membrane glycoprotein
XX CC GP1IIa/IIb and inhibits platelet agglutination. The Ig is thus
XX CC useful in the treatment of thrombosis.
XX SQ Sequence 214 AA;

Query Match 97.4%; Score 1089; DB 14; Length 214;
Best Local Similarity 96.7%; Pred. No. 1e-54;
Matches 207; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITCRASQDINNYLNWYQKPGKAPKLLIYTTSTLHSGVPS 60
DB 1 diqmtqspstlsasvgdrtvtitcrasqdinnynwyqkpgkapklllytstllhs9vps 60
QY 61 RFGSGSGTDYTLTISSLPQEDFATYYCQGGNTLPPTFGQGTKEIKRTVAAPSFIAPP 120
DB 61 rfsgsgsgtdytlttisslpqddfatyfcggntlpwtfgggtkveikrtvaapsvfifpp 120
QY 121 SDEQLKSGTASVCLLNFFYPREAKVQWKNALQSGNSQESVTQDSKDSYSLSTLT 180
DB 121 sdeqlksgtasvcllnffypreakvqwkvdnalqsgnsqesvteqgskdstyslsstlt 180
QY 181 LSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 214
DB 181 lskadyekhkvyacevthqglsspsvtksfnrgec 214

RESULT 13
AAR49815
ID AAR49815 standard; Protein; 214 AA.
XX
XX AAR49815;
XX AC
XX DT 24-SEP-1998 (first entry)
XX XX
XX DE Amino acid sequence of the humanised antibody C4G1 light chain.
XX XX
XX KW Humanised antibody C4G1; light chain; humanised; immunoglobulin; Ig;
XX KW mouse C4G1; antibody; inhibition; antigen; cardiovascular disease;
XX KW thromboembolic disorder; cancer; acute myocardial infarction;
XX KW unstable angina; stroke; transient ischemic episode; pulmonary embolism;
XX KW deep vein thrombosis; extracorporeal cardiopulmonary circulation.
```

```
XX Chimeric - Mus sp.
OS Chimeric - Homo sapiens.
XX US5777085-A.
XX 07-JUL-1998.
XX 17-MAY-1995; 95US-0458516.
XX 03-MAY-1993; 93US-0059159.
PR 20-DEC-1991; 91US-0812111.
PR 09-JUN-1992; 92US-0895952.
PR 11-SEP-1992; 92US-0944159.
XX (PROT-) PROTEIN DESIGN LABS INC.
XX Co MS, Tso JY;
XX WPI; 1998-398136/34.
XX New humanised immunoglobulin which binds GPIIb/IIIa - derived from
PT mouse C4G1 antibody, used for inhibiting platelet aggregation for
PT treating cardiovascular and thromboembolic disorders.
XX Claim 4; Fig 5C; 35pp; English.
XX This is the amino acid sequence of the humanised antibody C4G1 light
CC chain, used in the method of the invention involving the creation
CC of a humanised immunoglobulin (Ig) derived from the mouse C4G1 antibody.
CC The humanised Ig is capable of binding to GPIIb/IIIa and inhibiting
CC platelet aggregation and also the releasing reaction of platelets. The
CC Ig can be used for treating cardiovascular diseases and thromboembolic
CC disorders, e.g. acute myocardial infarction, unstable angina, stroke,
CC transient ischemic episodes, deep vein thrombosis and pulmonary embolism,
CC extracorporeal cardiopulmonary circulation. The Ig can also be used in
CC diagnosing the presence and location of a thrombus, or certain types of
CC cancer cells which develop GPIIb/IIIa on their surfaces, for the
CC detection of GPIIb/IIIa antigens or for isolating platelets.
XX Sequence 214 AA;
SQ
Query Match 97.4%; Score 1089; DB 19; Length 214;
Best Local Similarity 96.7%; Pred. No. 1e-54;
Matches 207; Conservative 6; Mismatches 1; Indels 0; Gaps 0;
QY 1 DIQWTQSPSLSASVGRVITICRASQDINNYLNWYQKPKAPKLLIYVSTLHSGVPS 60
DB 1 diqmtqtptstlsasvgrvdtiscrasqdinnlnwyqdkpgkapklliyvstlshgvsps 60
QY 61 RFGSGSGTDTYLTITISLQPEDFATYYCQCGNTLPPTFGQGTKEIKRTVAAPSVFIIPP 120
DB 61 rfgsgsgtdytltitisslqpddfatycqcgqntlpwtfggtkvekvrtvaapsvfifpp 120
QY 121 SDEQLKSGTASVCLLNFPYREAKVQWKVDNALQSGNSQESVTEQDSKDSYSLSTLT 180
DB 121 sdeqlksgtasvcllnfnfpreakvgkvkvdnalqsgnsqesvteqdsksdyslsstlt 180
QY 181 LSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 214
DB 181 lskadyekkhvyacevthqglsspvtksfnrgec 214
RESULT 14
AAV55078
ID AAY55078 standard; Protein; 367 AA.
XX
XX AAY55078;
XX
XX 25-QEB-2000 (first entry)
XX
XX Single chain Fv protein sequence shPW1-kappa.
```

```
XX Gene isolation; membrane-bound protein; fusion protein; drug production;
KW antigen-binding cell; secretable functional protein; antigenic protein;
KW protein isolation; diagnosis; ScFv.
XX Synthetic.
OS
PN WO9960113-A1.
XX
XX 25-NOV-1999.
XX
XX 30-APR-1999; 99WO-JP02341.
PF
XX
XX 20-MAY-1998; 98JP-0138652.
PR
XX 01-OCT-1998; 98JP-0279876.
PR
XX (CHUS ) CHUGAI SEIYAKU KK.
PA
XX
XX Tsuchiya M, Saito M, Ohtomo T;
XX
XX WPI; 2000-039382/03.
DR
XX N-PSDB; AA240308.
DR
XX Efficient and selective isolation of a gene encoding membrane protein
PT with low or no antigenic binding activity, for diagnosis, study of, and
PT production of drugs treating abnormal functions of the protein -
PT
XX
XX Example 7; Page 86-89; 120pp; Japanese.
PS
XX This sequence represents a single chain Fv (ScFv) sequence.
CC The invention relates to a method for isolating a gene encoding a
CC membrane-bound protein, comprising introducing a vector into a cell,
CC contacting an antigen with the cell expressing the fused protein encoded
CC by the vector on its surface to select an antigen-binding cell, and
CC isolating the cDNA. The vector contains DNA encoding a secretable
CC functional protein with antigenicity and binding affinity, and a cDNA
CC ligated to DNA downstream of the 3' end of the coding sequence. The
CC method can be used to isolate a membrane-bound protein for diagnosis and
CC study. It can also be used for producing drugs treating abnormal
CC functions of the protein. Such a technique is efficient and selective,
CC which is different from the prior-art transmembrane trap (TMT) method
CC wherein an epitope recognised by an antibody is carried in a fused
CC protein.
XX
XX Sequence 367 AA;
SQ
Query Match 95.6%; Score 1069; DB 21; Length 367;
Best Local Similarity 96.7%; Pred. No. 2.3e-53;
Matches 206; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
QY 1 DIQMTQSPSLSASVGRVITICRASQDINNYLNWYQKPKAPKLLIYVSTLHSGVPS 60
DB 154 diqmtqspslsasvgrvdtitcrasqdissylwnyqdkpgkapklliyvtsrlhsgvps 213
QY 61 RFGSGSGTDTYLTITISLQPEDFATYYCQCGNTLPPTFGQGTKEIKRTVAAPSVFIIPP 120
DB 214 rfgsgsgtdfttisslqpddiatyycqgntlpytfgggtkveikrtvaapsvfifpp 273
QY 121 SDEQLKSGTASVCLLNFPYREAKVQWKVDNALQSGNSQESVTEQDSKDSYSLSTLT 180
DB 274 sdeqlksgtasvcllnfnfpreakvgkvkvdnalqsgnsqesvteqdsksdyslsstlt 333
QY 181 LSKADYEKHKVYACEVTHQGLSSPVTKSFNRGE 213
DB 334 lskadyekkhvyacevthqglsspvtksfnrg 366
RESULT 15
AAV55081
ID AAY55081 standard; Protein; 626 AA.
XX
XX AAY55081;
AC
```

Search completed: August 14, 2002, 11:00:46
Job time: 527 sec

XX
DT 25-FEB-2000 (first entry)
XX
DE Single chain Fv protein sequence sHPW1-kappa-BvGS3.
XX
KW Gene isolation; membrane-bound protein; fusion protein; drug production;
KW antigen-binding cell; secretable functional protein; antigenic protein;
KW protein isolation; diagnosis; ScFv.
XX
OS Synthetic.
XX
PN WO960113-A1.
XX
PD 25-NOV-1999.
XX
PF 30-APR-1999; 99WO-JP02341.
XX
PR 20-MAY-1998; 98JP-0138652.
PR 01-OCT-1998; 98JP-0279876.
XX
PA (CHUS) CHUGAI SEIYAKU KK.
XX
PI Tsuchiya M, Saito M, Ohtomo T;
XX
DR WPI: 2000-039382/03.
DR N-PSDB; AAZ40316.
XX
PT Efficient and selective isolation of a gene encoding membrane protein
PT with low or no antigenic binding activity, for diagnosis, study of, and
PT production of drugs treating abnormal functions of the protein
XX
PS Example 7; Page 103-109; 120pp; Japanese.
XX
CC This sequence represents a single chain Fv (ScFv) sequence.
CC The invention relates to a method for isolating a gene encoding a
CC membrane-bound protein, comprising introducing a vector into a cell,
CC contacting an antigen with the cell expressing the fused protein encoded
CC by the vector on its surface to select an antigen-binding cell, and
CC isolating the cDNA. The vector contains DNA encoding a secretable
CC functional protein with antigenicity and binding affinity, and a cDNA
CC ligated to DNA downstream of the 3' end of the coding sequence. The
CC method can be used to isolate a membrane-bound protein for diagnosis and
CC study. It can also be used for producing drugs treating abnormal
CC functions of the protein. Such a technique is efficient and selective,
CC which is different from the prior-art transmembrane trap (TMT) method
CC wherein an epitope recognised by an antibody is carried in a fused
XX protein.
XX
SQ Sequence 626 AA;

Query Match 95.6%; Score 1069; DB 21; Length 626;
Best Local Similarity 96.7%; Pred. No. 3.6e-53;
Matches 206; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVITTCRASQDINNYLMWYQKPGKAPKLLIYYTSLHSGVPS 60
Db 413 diqmtqspsslsasvgrvittcrasqdisynlwyqkpgkpklliytsrlhsgvps 472
QY 61 RFGSGSGTDYTLTISSLPEDFATYYCOQGNLTLPPTFGQGTKEIKRTVAAPSVFIFPP 120
Db 473 rfgsgsgtdftfisslqpediatyycqgntlpytfggtkveikrtvaapsvfifpp 532
QY 121 SDEQLKSGTASVWCLLNFPYREAKVQWKVDNALQSGNSQESVTEQDSKDSFTYSLSSLT 180
Db 533 sdeqlksgtasvcllnfpypreakvqwkvdnalqsgnsqesvteqdsksdscysstlt 592
QY 181 LSKADYEKHYACEVTHQGLSSPVTKSFNRGE 213
Db 593 lskadyekhyacevthqglsspvtksfnrge 625

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 14, 2002, 11:01:12 ; Search time 20.83 seconds
(without alignments)
250.940 Million cell updates/sec

Title: US-09-811-384-11
Perfect score: 1118
Sequence: 1 DIQWQSPSLASVGDVTV.....EVTHQGLSSPVTKSFNRGEC 214

Scoring table: BLOSOM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : Issued Patents.AA.*
- 1: /cgn2_6/ptodata/2/1aa/5A_COMB.pep.*
 - 2: /cgn2_6/ptodata/2/1aa/5B_COMB.pep.*
 - 3: /cgn2_6/ptodata/2/1aa/6A_COMB.pep.*
 - 4: /cgn2_6/ptodata/2/1aa/6B_COMB.pep.*
 - 5: /cgn2_6/ptodata/2/1aa/PCTUS_COMB.pep.*
 - 6: /cgn2_6/ptodata/2/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1118	100.0	214	2 US-07-934-373C-40	Sequence 40, Appl
2	1118	100.0	214	2 US-08-788-800-11	Sequence 11, Appl
3	1118	100.0	214	3 US-08-437-642B-40	Sequence 40, Appl
4	1118	100.0	214	3 US-09-097-309-2	Sequence 2, Appl
5	1118	100.0	214	4 US-09-097-171A-2	Sequence 2, Appl
6	1118	100.0	214	5 PCT-US93-07832-40	Sequence 40, Appl
7	1118	100.0	233	2 US-07-934-373C-25	Sequence 25, Appl
8	1118	100.0	233	3 US-08-437-642B-25	Sequence 25, Appl
9	1118	100.0	233	5 PCT-US93-07832-25	Sequence 25, Appl
10	1118	100.0	237	3 US-09-097-309-6	Sequence 6, Appl
11	1118	100.0	237	4 US-09-097-171A-10	Sequence 10, Appl
12	1118	100.0	237	4 US-09-422-112B-2	Sequence 2, Appl
13	1118	100.0	237	4 US-09-607-756-2	Sequence 2, Appl
14	1110	99.3	214	2 US-07-934-373C-39	Sequence 39, Appl
15	1110	99.3	214	3 US-08-437-642B-39	Sequence 39, Appl
16	1110	99.3	214	5 PCT-US93-07832-39	Sequence 39, Appl
17	1089	97.4	214	1 US-08-458-516-12	Sequence 12, Appl
18	1035	92.6	214	2 US-07-934-373C-24	Sequence 24, Appl
19	1035	92.6	214	3 US-08-437-642B-24	Sequence 24, Appl
20	1035	92.6	214	5 PCT-US93-07832-24	Sequence 24, Appl
21	1031	92.2	214	4 US-09-679-397-1	Sequence 1, Appl
22	1031	92.2	237	2 US-08-463-587A-25	Sequence 25, Appl
23	1031	92.2	237	2 US-08-463-667A-3	Sequence 3, Appl
24	1031	92.2	237	3 US-08-923-854-25	Sequence 25, Appl
25	1031	92.2	237	5 PCT-US91-09133-26	Sequence 26, Appl
26	1024	91.6	214	1 US-08-425-763-1	Sequence 1, Appl
27	1024	91.6	214	3 US-08-811-757-1	Sequence 1, Appl

28	1024	91.6	214	4 US-09-249-230-1	Sequence 1, Appl
29	1021	91.3	218	5 PCT-US96-13152-2	Sequence 2, Appl
30	1016	90.9	218	2 US-08-887-352B-13	Sequence 13, Appl
31	1016	90.9	218	3 US-08-466-151-9	Sequence 9, Appl
32	1016	90.9	218	4 US-09-109-207C-13	Sequence 13, Appl
33	1016	90.9	218	4 US-09-296-005-13	Sequence 13, Appl
34	1016	90.9	218	4 US-08-466-163B-9	Sequence 9, Appl
35	1013	90.6	218	2 US-08-887-352B-15	Sequence 15, Appl
36	1013	90.6	218	2 US-08-887-352B-17	Sequence 17, Appl
37	1013	90.6	218	2 US-08-887-352B-19	Sequence 19, Appl
38	1013	90.6	218	2 US-08-887-352B-24	Sequence 24, Appl
39	1013	90.6	218	4 US-09-109-207C-15	Sequence 15, Appl
40	1013	90.6	218	4 US-09-109-207C-17	Sequence 17, Appl
41	1013	90.6	218	4 US-09-109-207C-19	Sequence 19, Appl
42	1013	90.6	218	4 US-09-109-207C-24	Sequence 24, Appl
43	1013	90.6	218	4 US-09-296-005-15	Sequence 15, Appl
44	1013	90.6	218	4 US-09-296-005-17	Sequence 17, Appl
45	1013	90.6	218	4 US-09-296-005-19	Sequence 19, Appl

ALIGNMENTS

RESULT 1
US-07-934-373C-40
; Sequence 40, Application US/07934373C
; Patent No. 5821337
; GENERAL INFORMATION:
; APPLICANT: Paul J. Carter
; APPLICANT: Leonard G. Presta
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/934,373C
; FILING DATE: 21-Aug-1992
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/05126
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 214 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-07-934-373C-40

Query Match 100.0%; Score 1118; DB 2; Length 214;
Best Local Similarity 100.0%; Pred. No. 1.5e-88;
Matches 214; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITCRASQDINNLYNNWYQOKPGKAPKLLIYYTSTLHSGVPS 60
DB 1 DIQMTQSPSSLSASVGDRTVITCRASQDINNLYNNWYQOKPGKAPKLLIYYTSTLHSGVPS 60
QY 61 RFGSGSGTDYTLTISLSLOPEDFATYYCOQGNTPPTFGQGTKEIKRTVAAPSVFIIPP 120
DB 61 RFGSGSGTDYTLTISLSLOPEDFATYYCOQGNTPPTFGQGTKEIKRTVAAPSVFIIPP 120
QY 121 SDEQLKSGTASVCLLNFFYPREKQVQKVDNALQSGNSQESVTEQDSKSTYLSLSTLT 180
DB 121 SDEQLKSGTASVCLLNFFYPREKQVQKVDNALQSGNSQESVTEQDSKSTYLSLSTLT 180
QY 181 LSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 214
DB 181 LSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 214
RESULT 2
US-08-788-800-11
; Sequence 11, Application US/08788800
; Patent No. 5914112
; GENERAL INFORMATION:
; APPLICANT: Bednar, Martin M.
; APPLICANT: Thomas, G. Roger
; APPLICANT: Gross, Cordell E.
; TITLE OF INVENTION: ANTI-CD18 ANTIBODIES IN STROKE
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/788,800
; FILING DATE: 22-Jan-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0987r1
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 214 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-788-800-11

Query Match 100.0%; Score 1118; DB 2; Length 214;
Best Local Similarity 100.0%; Pred. No. 1.5e-88;
Matches 214; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITCRASQDINNLYNNWYQOKPGKAPKLLIYYTSTLHSGVPS 60
DB 1 DIQMTQSPSSLSASVGDRTVITCRASQDINNLYNNWYQOKPGKAPKLLIYYTSTLHSGVPS 60
QY 61 RFGSGSGTDYTLTISLSLOPEDFATYYCOQGNTPPTFGQGTKEIKRTVAAPSVFIIPP 120
DB 61 RFGSGSGTDYTLTISLSLOPEDFATYYCOQGNTPPTFGQGTKEIKRTVAAPSVFIIPP 120
QY 121 SDEQLKSGTASVCLLNFFYPREKQVQKVDNALQSGNSQESVTEQDSKSTYLSLSTLT 180
DB 121 SDEQLKSGTASVCLLNFFYPREKQVQKVDNALQSGNSQESVTEQDSKSTYLSLSTLT 180

DB 121 SDEQLKSGTASVCLLNFFYPREKQVQKVDNALQSGNSQESVTEQDSKSTYLSLSTLT 180
QY 181 LSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 214
DB 181 LSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 214
RESULT 3
US-08-437-642B-40
; Sequence 40, Application US/08437642B
; Patent No. 6054297
; GENERAL INFORMATION:
; APPLICANT: Paul J. Carter
; APPLICANT: Leonard G. Presta
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/437,642B
; FILING DATE: 09-May-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/934373
; FILING DATE: 21-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/146206
; FILING DATE: 17-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/05126
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P2C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 214 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-437-642B-40

Query Match 100.0%; Score 1118; DB 3; Length 214;
Best Local Similarity 100.0%; Pred. No. 1.5e-88;
Matches 214; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITCRASQDINNLYNNWYQOKPGKAPKLLIYYTSTLHSGVPS 60
DB 1 DIQMTQSPSSLSASVGDRTVITCRASQDINNLYNNWYQOKPGKAPKLLIYYTSTLHSGVPS 60
QY 61 RFGSGSGTDYTLTISLSLOPEDFATYYCOQGNTPPTFGQGTKEIKRTVAAPSVFIIPP 120
DB 61 RFGSGSGTDYTLTISLSLOPEDFATYYCOQGNTPPTFGQGTKEIKRTVAAPSVFIIPP 120
QY 121 SDEQLKSGTASVCLLNFFYPREKQVQKVDNALQSGNSQESVTEQDSKSTYLSLSTLT 180
DB 121 SDEQLKSGTASVCLLNFFYPREKQVQKVDNALQSGNSQESVTEQDSKSTYLSLSTLT 180

Db 121 SDEQLKSGTASVVCLLNFPYPREAKVQKVDNALQSGNSQESVTEQDSKDYSLSTLT 180
QY 181 LSKADYERKHKYACVETHQGLSSPVTKSFNRGEC 214
Db 181 LSKADYERKHKYACVETHQGLSSPVTKSFNRGEC 214

RESULT 4
US-09-097-309-2
; Sequence 2, Application US/09097309
; Patent No. 6121428
; GENERAL INFORMATION:
; APPLICANT: Blank, Gregory S.
; APPLICANT: Narindray, Daljit S.
; APPLICANT: Zapata, Gerardo A.
; TITLE OF INVENTION: Protein Recovery
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/097,309
; FILING DATE: 12-Jun-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/050951
; FILING DATE: 13-JUN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Schwartz, Timothy R.
; REGISTRATION NUMBER: 32171
; REFERENCE/DOCKET NUMBER: P1105R1
; TELEPHONE: 650/225-7467
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 214 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-09-097-309-2

Query Match 100.0%; Score 1118; DB 3; Length 214;
Best Local Similarity 100.0%; Pred. No. 1.5e-88;
Matches 214; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITCRASQDINNYLNWYQKPGKAPKLLIYYTSTLHSGVPS 60
Db 1 DIQMTQSPSSLSASVGDRTVITCRASQDINNYLNWYQKPGKAPKLLIYYTSTLHSGVPS 60

QY 61 RFGSGSGTDYTLTISSLPQEDFATYYCQGNLTLPPTFGQGTKEIKRTVAAPSVFIAPP 120
Db 61 RFGSGSGTDYTLTISSLPQEDFATYYCQGNLTLPPTFGQGTKEIKRTVAAPSVFIAPP 120

QY 121 SDEQLKSGTASVVCLLNFPYPREAKVQKVDNALQSGNSQESVTEQDSKDYSLSTLT 180
Db 121 SDEQLKSGTASVVCLLNFPYPREAKVQKVDNALQSGNSQESVTEQDSKDYSLSTLT 180

QY 181 LSKADYERKHKYACVETHQGLSSPVTKSFNRGEC 214
Db 181 LSKADYERKHKYACVETHQGLSSPVTKSFNRGEC 214

RESULT 5
PCT-US93-07832-40
; Sequence 40, Application PC/TUS9307832
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.

US-09-097-171A-2
; Sequence 2, Application US/09097171A
; Patent No. 6171586
; GENERAL INFORMATION:
; APPLICANT: Lam, Xanthe M.
; APPLICANT: Oeswein, James Q.
; APPLICANT: Ongpipattanakul, Boonsri
; APPLICANT: Shahrokh, Zahra
; APPLICANT: Wang, Sharon X.
; APPLICANT: Weissburg, Robert P.
; APPLICANT: Wong, Rita L.
; TITLE OF INVENTION: Antibody Formulation
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/097,171A
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/874897
; FILING DATE: 13-JUN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P1089R1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 214 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-09-097-171A-2

Query Match 100.0%; Score 1118; DB 4; Length 214;
Best Local Similarity 100.0%; Pred. No. 1.5e-88;
Matches 214; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITCRASQDINNYLNWYQKPGKAPKLLIYYTSTLHSGVPS 60
Db 1 DIQMTQSPSSLSASVGDRTVITCRASQDINNYLNWYQKPGKAPKLLIYYTSTLHSGVPS 60

QY 61 RFGSGSGTDYTLTISSLPQEDFATYYCQGNLTLPPTFGQGTKEIKRTVAAPSVFIAPP 120
Db 61 RFGSGSGTDYTLTISSLPQEDFATYYCQGNLTLPPTFGQGTKEIKRTVAAPSVFIAPP 120

QY 121 SDEQLKSGTASVVCLLNFPYPREAKVQKVDNALQSGNSQESVTEQDSKDYSLSTLT 180
Db 121 SDEQLKSGTASVVCLLNFPYPREAKVQKVDNALQSGNSQESVTEQDSKDYSLSTLT 180

QY 181 LSKADYERKHKYACVETHQGLSSPVTKSFNRGEC 214
Db 181 LSKADYERKHKYACVETHQGLSSPVTKSFNRGEC 214

RESULT 6
PCT-US93-07832-40
; Sequence 40, Application PC/TUS9307832
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.

ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/437.642B
FILING DATE: 09-May-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/934373
FILING DATE: 21-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/146206
FILING DATE: 17-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/15272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709P2C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 233 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-437-642B-25

Query Match 100.0%; Score 1118; DB 3; Length 233;
Best Local Similarity 100.0%; Pred. No. 1.7e-88;
Matches 214; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DIQMTQSPSSLSASVGRVTITCRASQDINNYLNWYQKPGKAPKLLIYYTSTLHSGVPS 60
Db 20 DIQMTQSPSSLSASVGRVTITCRASQDINNYLNWYQKPGKAPKLLIYYTSTLHSGVPS 79
QY 61 RFGSGSGTDYTLTISSLPQEDFATYYCQGNLPPPTFGQGTKEIKRTVAAPSVFIFPP 120
Db 80 RFGSGSGTDYTLTISSLPQEDFATYYCQGNLPPPTFGQGTKEIKRTVAAPSVFIFPP 139
QY 121 SDEQLKSGTASVVCVLLNFPYKQVQKVDNALQSGNSQESVTEQDSKDSSTLT 180
Db 140 SDEQLKSGTASVVCVLLNFPYKQVQKVDNALQSGNSQESVTEQDSKDSSTLT 199
QY 181 LSKADYEKKHYACEVTHQGLSSPVTKSFNRGEC 214
Db 200 LSKADYEKKHYACEVTHQGLSSPVTKSFNRGEC 233

RESULT 9
PCT-US93-07832-25
Sequence 25, Application PC/TUS9307832
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:

MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/07832
FILING DATE: 19930820
CLASSIFICATION:
PRIOR APPLICATION DATA: 07/715272
FILING DATE: 14-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA: 07/934373
FILING DATE: 21-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME:
REGISTRATION NUMBER:
REFERENCE/DOCKET NUMBER: 709P2PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE:
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 233 amino acids
TYPE: amino acid
TOPOLOGY: linear
PCT-US93-07832-25

Query Match 100.0%; Score 1118; DB 5; Length 233;
Best Local Similarity 100.0%; Pred. No. 1.7e-88;
Matches 214; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DIQMTQSPSSLSASVGRVTITCRASQDINNYLNWYQKPGKAPKLLIYYTSTLHSGVPS 60
Db 20 DIQMTQSPSSLSASVGRVTITCRASQDINNYLNWYQKPGKAPKLLIYYTSTLHSGVPS 79
QY 61 RFGSGSGTDYTLTISSLPQEDFATYYCQGNLPPPTFGQGTKEIKRTVAAPSVFIFPP 120
Db 80 RFGSGSGTDYTLTISSLPQEDFATYYCQGNLPPPTFGQGTKEIKRTVAAPSVFIFPP 139
QY 121 SDEQLKSGTASVVCVLLNFPYKQVQKVDNALQSGNSQESVTEQDSKDSSTLT 180
Db 140 SDEQLKSGTASVVCVLLNFPYKQVQKVDNALQSGNSQESVTEQDSKDSSTLT 199
QY 181 LSKADYEKKHYACEVTHQGLSSPVTKSFNRGEC 214
Db 200 LSKADYEKKHYACEVTHQGLSSPVTKSFNRGEC 233

RESULT 10
US-09-097-309-6
Sequence 6, Application US/09097309
Patent No. 6121428
GENERAL INFORMATION:
APPLICANT: Blank, Gregory S.
APPLICANT: Narindray, Daljit S.
APPLICANT: Zapata, Gerardo A.
TITLE OF INVENTION: Protein Recovery
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/097,309
; FILING DATE: 12-Jun-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/050951
; FILING DATE: 13-JUN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Schwartz, Timothy R.
; REGISTRATION NUMBER: 32171
; REFERENCE/DOCKET NUMBER: P1105R1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-7467
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 237 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-09-097-309-6

Query Match 100.0%; Score 1118; DB 3; Length 237;
Best Local Similarity 100.0%; Pred. No. 1.7e-88;
Matches 214; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTTTCRASQDINNLYNWYQKPGKAPKLLIYYTSTLHSGVPS 60
Db 24 DIQMTQSPSSLSASVGRVTTTCRASQDINNLYNWYQKPGKAPKLLIYYTSTLHSGVPS 83

QY 61 RFSGSGSGTDYTLTISSLPQEDFATYYCQOGNTLPTTFGGQTKVEIKRTVAAPSVFIFPP 120
Db 84 RFSGSGSGTDYTLTISSLPQEDFATYYCQOGNTLPTTFGGQTKVEIKRTVAAPSVFIFPP 143

QY 121 SDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYLSSTLT 180
Db 144 SDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYLSSTLT 203

QY 181 LSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 214
Db 204 LSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 237

RESULT 11
US-09-097-171A-10
; Sequence 10, Application US/09097171A
; Patent No. 6171586
; GENERAL INFORMATION:
; APPLICANT: Lam, Xanthe M.
; APPLICANT: Oeswein, James Q.
; APPLICANT: Ongpipattanakul, Boonsri
; APPLICANT: Shahrokh, Zahra
; APPLICANT: Wang, Sharon X.
; APPLICANT: Weissburg, Robert P.
; APPLICANT: Wong, Rita L.
; TITLE OF INVENTION: Antibody Formulation
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech),
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/097,171A
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/874897
; FILING DATE: 13-JUN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P1089R1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 237 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-09-097-171A-10

Query Match 100.0%; Score 1118; DB 4; Length 237;
Best Local Similarity 100.0%; Pred. No. 1.7e-88;
Matches 214; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTTTCRASQDINNLYNWYQKPGKAPKLLIYYTSTLHSGVPS 60
Db 24 DIQMTQSPSSLSASVGRVTTTCRASQDINNLYNWYQKPGKAPKLLIYYTSTLHSGVPS 83

QY 61 RFSGSGSGTDYTLTISSLPQEDFATYYCQOGNTLPTTFGGQTKVEIKRTVAAPSVFIFPP 120
Db 84 RFSGSGSGTDYTLTISSLPQEDFATYYCQOGNTLPTTFGGQTKVEIKRTVAAPSVFIFPP 143

QY 121 SDQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYLSSTLT 180
Db 144 SDQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYLSSTLT 203

QY 181 LSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 214
Db 204 LSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 237

RESULT 12
US-09-422-712B-2
; Sequence 2, Application US/09422712B
; Patent No. 6180367
; GENERAL INFORMATION:
; APPLICANT: Leung, Moon-Lam Susan
; APPLICANT: Swartz, James R.
; TITLE OF INVENTION: PROCESS FOR BACTERIAL PRODUCTION OF POLYPEPTIDES
; FILE REFERENCE: P1711R1
; CURRENT APPLICATION NUMBER: US/09/422,712B
; CURRENT FILING DATE: 1999-10-21
; NUMBER OF SEQ ID NOS: 4
; SEQ ID NO 2
; LENGTH: 237
; TYPE: PRT
; ORGANISM: Human
US-09-422-712B-2

Query Match 100.0%; Score 1118; DB 4; Length 237;
Best Local Similarity 100.0%; Pred. No. 1.7e-88;
Matches 214; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTTTCRASQDINNLYNWYQKPGKAPKLLIYYTSTLHSGVPS 60
Db 24 DIQMTQSPSSLSASVGRVTTTCRASQDINNLYNWYQKPGKAPKLLIYYTSTLHSGVPS 83

QY 61 RFSGSGSGTDYTLTISSLPQEDFATYYCQOGNTLPTTFGGQTKVEIKRTVAAPSVFIFPP 120
Db 84 RFSGSGSGTDYTLTISSLPQEDFATYYCQOGNTLPTTFGGQTKVEIKRTVAAPSVFIFPP 143

QY 121 SDEQLKSGTASVWCLLNFFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYSLSTLT 180
Db 144 SDEQLKSGTASVWCLLNFFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYSLSTLT 203
QY 181 LSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 214
Db 204 LSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 237

RESULT 13
US-09-607-756-2
; Sequence 2, Application US/09607756
; Patent No. 6258560
; GENERAL INFORMATION:
; APPLICANT: Leung, Woon-Lam Susan
; APPLICANT: Swartz, James R.
; TITLE OF INVENTION: PROCESS FOR BACTERIAL PRODUCTION OF POLYPEPTIDES
; FILE REFERENCE: P1711R1
; CURRENT APPLICATION NUMBER: US/09/607,756
; CURRENT FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: US 09/422,712
; PRIOR FILING DATE: 1999-10-21
; NUMBER OF SEQ ID NOS: 4
; SEQ ID NO 2
; LENGTH: 237
; TYPE: PRT
; ORGANISM: Human
US-09-607-756-2

Query Match 100.0%; Score 1118; DB 4; Length 237;
Best Local Similarity 100.0%; Pred. No. 1.7e-88;
Matches 214; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCRASQDINNYLNWYQKPKAPKLLIYTTSLHSGVPS 60
Db 24 DIQMTQSPSSLSASVGRVTITCRASQDINNYLNWYQKPKAPKLLIYTTSLHSGVPS 83
QY 61 RFGSGSGTDYTLTISSLPQEDFATYYCOQGNLPPPTFGQGTKEIKRTVAAPSFIIPP 120
Db 84 RFGSGSGTDYTLTISSLPQEDFATYYCOQGNLPPPTFGQGTKEIKRTVAAPSFIIPP 143
QY 121 SDEQLKSGTASVWCLLNFFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYSLSTLT 180
Db 144 SDEQLKSGTASVWCLLNFFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYSLSTLT 203
QY 181 LSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 214
Db 204 LSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 237

RESULT 14
US-07-934-373C-39
; Sequence 39, Application US/07934373C
; Patent No. 5821337
; GENERAL INFORMATION:
; APPLICANT: Paul J. Carter
; APPLICANT: Leonard G. Presta
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/437,642B
; FILING DATE: 09-May-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/934373
; FILING DATE: 21-AUG-1992

; APPLICATION NUMBER: US/07/934,373C
; FILING DATE: 21-Aug-1992
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/05126
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/228-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 214 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-07-934-373C-39

Query Match 99.3%; Score 1110; DB 2; Length 214;
Best Local Similarity 99.5%; Pred. No. 7.4e-88;
Matches 213; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCRASQDINNYLNWYQKPKAPKLLIYTTSLHSGVPS 60
Db 1 DIQMTQSPSSLSASVGRVTITCRASQDINNYLNWYQKPKAPKLLIYTTSLHSGVPS 60
QY 61 RFGSGSGTDYTLTISSLPQEDFATYYCOQGNLPPPTFGQGTKEIKRTVAAPSFIIPP 120
Db 61 RFGSGSGTDYTLTISSLPQEDFATYYCOQGNLPPPTFGQGTKEIKRTVAAPSFIIPP 120
QY 121 SDQLKSGTASVWCLLNFFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYSLSTLT 180
Db 121 SDQLKSGTASVWCLLNFFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYSLSTLT 180
QY 181 LSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 214
Db 181 LSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 214

RESULT 15
US-08-437-642B-39
; Sequence 39, Application US/08437642B
; Patent No. 6054297
; GENERAL INFORMATION:
; APPLICANT: Paul J. Carter
; APPLICANT: Leonard G. Presta
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/437,642B
; FILING DATE: 09-May-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/934373
; FILING DATE: 21-AUG-1992

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/146206
; FILING DATE: 17-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/05126
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P2C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 214 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-437-642B-39

Query Match 99.3%; Score 1110; DB 3; Length 214;
Best Local Similarity 99.5%; Pred. No. 7.4e-88;
Matches 213; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITCRASQDINNLYNMYQKPKAPKLLIYYTSTLHSGVPS 60
Db 1 DIQMTQSPSSLSASVGDRTVITCRASQDINNLYNMYQKPKAPKLLIYYTSTLHSGVPS 60

QY 61 RFGSGSGTDYTLTISSLPEDFATYYCQGGNTLPPTFGQGTKVEIKRTVAAPSVFIFPP 120
Db 61 RFGSGSGTDYTLTISSLPEDFATYYCQGGNTLPPTFGQGTKVEIKRTVAAPSVFIFPP 120

QY 121 SDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYLSSTLT 180
Db 121 SDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYLSSTLT 180

QY 181 LSKADYEKKHYACEVTHQGLSSPVTKSFNRGEC 214
Db 181 LSKADYEKKHYACEVTHQGLSSPVTKSFNRGEC 214

Search completed: August 14, 2002, 11:01:13
Job time: 238 sec